DETECTION AND MODULATION OF IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE DISEASE

Cross-reference to Related Applications

This Application is a continuation application of U.S.S.N. 09/617,053, filed July 14, 2000 (now allowed), which is a continuation application of U.S.S.N. 08/800,929, filed February 13, 1997 (now U.S. Patent No. 6,133,437).

Background of the Invention

The invention relates to the diagnosis and treatment of cancer.

One way by which cells die is referred to as apoptosis, or programmed cell death. Apoptosis often occurs as a normal part of the development and maintenance of health tissues. The process occurs so rapidly that it is difficult to detect. This may help to explain why the involvement of apoptosis in a wide spectrum of biological processes has only recently been recognized.

The apoptosis pathway is now known to play a critical role in embryonic development, viral pathogenesis, cancer, autoimmune disorders, and neurodegenerative disease. The failure of an apoptotic response has been implicated in the development of cancer, autoimmune disorders, such as lupus erythematosis and multiple sclerosis, and in viral infections, including those associated with herpes virus, poxvirus, and adenovirus.

Baculoviruses encode proteins that are termed inhibitors of apoptosis proteins (IAPs) because they inhibit the apoptosis that would otherwise occur

when insect cells are infected by the virus. These proteins are thought to work in a manner that is independent of other viral proteins. The baculovirus IAP genes include sequences encoding a ring zinc finger-like motif (RZF), which is presumed to be directly involved in DNA binding, and two N-terminal domains that consist of a 70 amino acid repeat motif termed a BIR domain (Baculovirus IAP Repeat).

The role of apoptosis in cancer has only recently been appreciated. The identification of growth promoting "oncogenes" in the late 1970's gave rise to an almost universal focus on cellular proliferation that dominated research in cancer biology for many years. Long-standing dogma held that anti-cancer therapies preferentially targeted rapidly dividing cancer cells relative to "normal" cells. This explanation was not entirely satisfactory, since some slow growing tumors are easily treated, while many rapidly dividing tumor types are extremely resistant to anti-cancer therapies. Progress in the cancer field has now led to a new paradigm in cancer biology wherein neoplasia is viewed as a failure to execute normal pathways of programmed cell death. Normal cells receive continuous feedback from their neighbors through various growth factors, and commit "suicide" if removed from this context. Cancer cells somehow ignore these commands and continue inappropriate proliferation. Cancer therapies, including radiation and many chemotherapies, have traditionally been viewed as causing overwhelming cellular injury. New evidence suggests that cancer therapies actually work by triggering apoptosis.

Both normal cell types and cancer cell types display a wide range of susceptibility to apoptotic triggers, although the determinants of this resistance are only now under investigation. Many normal cell types undergo temporary growth

arrest in response to a sub-lethal dose of radiation or cytotoxic chemical, while cancer cells in the vicinity undergo apoptosis. This provides the crucial treatment "window" of appropriate toxicity that allows successful anti-cancer therapy. It is therefore not surprising that resistance of tumor cells to apoptosis is emerging as a major category of cancer treatment failure.

Compared to the numerous growth promoting oncogenes identified to date (>100) relatively few genes have been isolated that regulate apoptosis. The Bcl-2 gene was first identified as an oncogene associated with the development of follicular lymphomas. In contrast to all other oncogenes identified to date, Bcl-2 displays no ability to promote cell proliferation, and instead has been demonstrated to suppress apoptosis by a variety of triggers. Elevated bcl-2 expression is associated with a poor prognosis in neuroblastoma, prostate and colon cancer, and can result in a multidrug resistant phenotype *in vitro*. Although the study of Bcl-2 has helped revolutionize cancer paradigms, the vast majority of human malignancies do not demonstrate aberrant Bcl-2 expression.

In contrast to the findings with bcl-2, mutation of the p53 tumor suppresser gene has been estimated to occur in up to 50% of human cancers and is the most frequent genetic change associated with cancer to date. The p53 protein plays a crucial role in surveying the genome for DNA damage. The cell type and degree of damage determines whether the cell will undergo growth arrest and repair, or initiate apoptosis. Mutations in p53 interfere with this activity, rendering the cell resistant to apoptosis by a wide range of cellular insults. Some progress has been made in understanding the molecular biology of p53, but many questions remain. p53 is known to function as a transcription factor, with the ability to positively or negatively regulate the expression of a variety of genes

involved in cell cycle control, DNA repair, and apoptosis (including the anti-apoptotic Bcl-2 gene described above and the related proapoptotic gene bax). The drug resistant phenotype conferred by p53 alterations has been linked to Bcl-2/Bax regulation, but this correlation does not hold for most cancer types, leaving open the possibility that other critical genes regulated by p53 remain to be identified.

Summary of the Invention

We have discovered that IAP and NAIP overexpression are associated with a wide range of cancer types including ovarian cancer, adenocarcinoma, lymphoma, and pancreatic cancer. In addition, we have found that nuclear localization fragmentation of the IAPs, and overexpression of the IAPs in the presence of p53 mutations correlate with a cancer diagnosis, a poor prognosis, and resistance to numerous chemotherapeutic cancer drugs. These discoveries provide diagnostic, prognostic, and therapeutic compounds and methods for the detection and treatment of proliferative diseases.

In the first aspect, the invention features a method of detecting cancer or an increased likelihood of cancer by detecting an increase IAP gene expression or protein expression in a cell from the mammal. In various embodiments, the detection may be performed by contacting with IAP or NAIP nucleic acid, or a portion thereof (which is greater than 9 nucleotides, and preferably greater than 18 nucleotides in length), with a preparation of nucleic acid from the cell; detecting levels of IAP or NAIP nucleic acid using quantitative nucleic acid amplification techniques; monitoring the levels of IAP or NAIP protein; or monitoring the levels of IAP or NAIP biological activity. Preferably, the cell is a cell from a mammal

suspected of having a leukemia, a lymphoma, breast cancer, pancreatic cancer, melanoma, lung cancer, or ovarian cancer.

In one embodiment utilizing nucleic acid amplification for detection, the invention features characterization of a cellular IAP or NAIP nucleic acid content and levels by: (a) providing a sample of nucleic acid; (b) providing a pair of oligonucleotides having sequence homology to an IAP or NAIP nucleic acid; (c) combining the pair of oligonucleotides with the cellular sample under conditions suitable for polymerase chain reaction-mediated nucleic acid amplification; and (d) isolating the amplified IAP nucleic acid or fragment thereof. The isolated nucleic acid may then be quantitated, sequenced, or otherwise characterized for the activity it imparts on the cell or related cells. In preferred embodiments, the amplification is carried out using a reverse-transcription polymerase chain reaction, for example, the RACE method.

In one embodiment using nucleic acid hybridization for detection, the invention features use of IAP or NAIP nucleic acid isolated according to the method involving: (a) providing a preparation of nucleic acid; (b) providing a detectably-labelled nucleotide sequence having homology to a region of an IAP or NAIP nucleic acid; (c) contacting the preparation of nucleic acid with the detectably-labelled nucleic acid sequence under hybridization conditions providing detection of nucleic acid having 50% or greater nucleotide sequence identity; and (d) identifying IAP or NAIP and characterizing nucleic acid by their association with the detectable label.

In one embodiment utilizing antibodies for detection, the invention features methods for using a purified antibody that binds specifically to an IAP or NAIP family of proteins. Such an antibody may be used for diagnosis and also for

drug screens, prognostic methods, and treatment methods described herein. Any standard immunodetection method may be employed, as appropriate. Preferably, the antibody binds specifically to XIAP, HIAP-1, HIAP-2 or NAIP. In various embodiments, the antibody may react with other IAP polypeptides or may be specific for one or a few IAP polypeptides. The antibody may be a monoclonal or a polyclonal antibody. Preferably, the antibody reacts specifically with only one of the IAP polypeptides, for example, reacts with murine and human xiap, but not with hiap-1 or hiap-2 from other mammalian species. In any of the immunodetection, diagnostic and prognostic methods an increase in IAP or NAIP polypeptide levels or an increase in the level of certain IAP or NAIP fragments described herein (e.g., BIR-containing fragments or nuclear polypeptides, found to be associated with proliferation indicate a cancer diagnosis or a poor cancer prognosis when therapeutics which act by enhancing apoptosis are used for treatment.

In another aspect, the invention features a IAP or NAIP gene nucleic acid fragment or antisense RNA sequence for use in suppressing cell proliferation. Such nucleic acids of the invention and methods for using them may be identified according to a method involving: (a) providing a cell sample; (b) introducing by transformation into the cell sample a candidate IAP or NAIP nucleic acid; (c) expressing the candidate IAP or NAIP nucleic acid within the cell sample; and (d) determining whether the cell sample exhibits an altered apoptotic response, whereby decreased apoptosis identifies an anti-proliferative compound. Preferably, the cell is a cancer cell.

In another aspect, the invention features a method of determining the prognosis of a mammal having a proliferative disease. The method includes

detecting levels of IAP or NAIP nucleic acids, protein levels, or biological activity, or IAP fragments in the cell suspected to be involved in a proliferative disease. In various embodiments, the methods of detection described above for diagnosis may be employed. An increase in IAP or NAIP levels indicates a proliferative disease (i.e., an increased likelihood the cancers described herein) and, particularly if a p53 mutation is present, a poor prognosis for therapeutic approaches which rely on enhancing apoptosis. The presence of IAP fragments of less than 64 kD, more preferably less than 45 kD indicates in increased likelihood that the cancer will be resistant to chemotherapeutics which act by inducing apoptosis.

In preferred embodiments of the diagnostic and prognostic methods, the levels being monitored are levels of IAP or NAIP express or activity levels known to be associated with cancer suspected or diagnosed. Most preferably, the disease is selected from the group consisting of a breast cancer (preferably using a hiap-2, hiap-1, HIAP-2, or HIAP-1 probe), ovarian cancer (preferably using a hiap-2, or HIAP-2 probe), promyelocytic leukemia, a HeLa-type carcinoma, chronic myelogenous leukemia (preferably using a xiap, hiap-2, XIAP or HIAP-2 probe), lymphoblastic leukemia (preferably using a xiap or XIAP probes), Burkitt's lymphoma (preferably using a hiap-1 or HIAP-1 probe), colorectal adenocarcinoma, lung carcinoma, and melanoma (preferably using a xiap, or XIAP probe). Preferably, a cancer diagnosis or poor prognosis is indicated by a 2-fold increase in expression or activity, more preferably, at least a 10-fold increase in expression or activity in the cell being tested.

In another aspect, the invention features a method of identifying a compound that inhibits cancer by enhancing apoptosis. The method includes

providing a cell expressing an IAP or NAIP polypeptide and being capable of proliferation or viability in culture, contacting the cell with a candidate compound, and monitoring the expression of an IAP gene, NAIP gene, a reporter linked to IAP or NAIP regulatory sequence, levels of IAP or NAIP polypeptides, cleavage of IAP polypeptides, and/or nuclear versus cytoplasmic localization of IAP or NAIP polypeptides. A decrease in the level of expression of the IAP or NAIP gene, IAP or NAIP protein characteristics, IAP or NAIP biological activity, IAP cleavage, or localization of protein to the nucleus, indicate the presence of a compound which enhances apoptosis, as described herein. In various preferred embodiments, the cell used in the method is a fibroblast, a neuronal cell, a glial cell, a lymphocyte (T cell or B cell), a breast cancer cell, a lymphoma cell, an ovarian cancer cell, a leukemia cell, a pancreatic cancer cell, a melanoma cell, or an insect cell; the preferred polypeptide expression being monitored is XIAP, HIAP-1, HIAP-2, or NAIP (i.e., human or murine). In the embodiment utilizing fragment detection, the fragment is preferably less than 64 kD, more preferably less than 45 kD. All the detection methods described herein may be employed, as appropriate.

In a related aspect, the invention features methods of detecting compounds that enhance apoptosis using the interaction trap technology and IAP or NAIP polypeptides, or fragments thereof, as a component of the bait. In preferred embodiments, the compound being tested as an enhancer of apoptosis is also a polypeptide.

In another aspect, the invention features a method of treating a patient diagnosed with a proliferative disease. In the method, apoptosis may be induced in a cell to control a proliferative disease either alone or in combination

with other therapies by administering to the cell a negative regulator of the IAP-dependent or NAIP anti-apoptotic pathway. The negative regulator may be, but is not limited to, an IAP ring zinc finger, and an IAP polypeptide that includes a ring zinc finger and lacks at least one BIR domain. Alternatively, apoptosis may be induced in the cell by administering a nucleic acid encoding an IAP antisense RNA molecule administered directly or via gene therapy (see U.S. Pat. No. 5,576,208 for general parameters which may be applicable in the selection of IAP or NAIP antisense RNAs). In yet another method, the negative regulator may be a purified antibody, or a fragment thereof, that binds specifically to an IAP polypeptide. For example, in one preferred embodiment, the antibody may bind to an approximately 26 kDa cleavage product of an IAP polypeptide that includes at least one BIR domain but lacks a ring zinc finger domain.

In two additional aspects, the invention features a transgenic animal and methods of using the mammal for detection of anti-cancer therapeutics. Preferably the mammal overexpresses an IAP or NAIP polypeptide and/or expresses a NAIP or IAP antisense RNA or IAP or NAIP fragment. In one embodiment, the animal also has a genetic predisposition to cancer or has cancer cells under conditions which provide for proliferation absent the transgenic construct encoding either the antisense RNA or fragment.

By "IAP gene" is meant a gene encoding a polypeptide having at least one BIR domain and a ring zinc finger domain which is capable of modulating (inhibiting or enhancing) apoptosis in a cell or tissue when provided by other intracellular or extracellular delivery methods (see, e.g., U.S.S.Ns. 08/511,485, 08/576,965, and PCT/IB96/01022). In preferred embodiments the IAP gene is a gene having about 50% or greater nucleotide sequence identity to at

least one of the IAP amino acid encoding sequences of Figs. 1-4 or portions thereof. Preferably, the region of sequence over which identity is measured is a region encoding at least one BIR domain and a ring zinc finger domain. Mammalian IAP genes include nucleotide sequences isolated from any mammalian source. Preferably, the mammal is a human. The term "IAP gene" is meant to encompass any member of the family of genes that encode inhibitors of apoptosis. An IAP gene may encode a polypeptide that has at least 20%, preferably at least 30%, and most preferably at least 50% amino acid sequence identity with at least one of the conserved regions of one of the IAP members described herein (i.e., either the BIR or ring zinc finger domains from the human or murine xiap, hiap-1 and hiap-2). Representative members of the IAP gene family include, without limitation, the human and murine xiap, hiap-1, and hiap-2 genes.

By "IAP protein" or "IAP polypeptide" is meant a polypeptide, or fragment thereof, encoded by an IAP gene.

"NAIP gene" and "NAIP polypeptide" means the NAIP genes, fragments thereof, and polypeptides encoded by the same described in UK9601108.5 filed January 19, 1996 and the PCT application claiming priority from UK9601108.5 filed January 17, 1997.

By "BIR domain" is meant a domain having the amino acid sequence of the consensus sequence: Xaal-Xaal-Xaal-Arg-Leu-Xaal-Thr-Phe-Xaal-Xaal-Trp-Pro-Xaa2-Xaal-Xaal-Xaa2-Xaa2-Xaal-Xaal-Xaal-Xaal-Leu-Ala-Xaal-Ala-Gly-Phe-Tyr-Tyr-Xaal-Gly-Xaal-Xaal-Asp-Xaal-Val-Xaal-Cys-Phe-Xaal-Cys-Xaal-Xaal- Xaal-Xaal-Xaal-Xaal-Trp-Xaal-Xaal-Xaal-Asp-Xaal-Xaal-Xaal- Xaal-Xaal-His-Xaal-Xaal-Xaal-Xaal-Pro-Xaal-Cys-Xaal-Phe-Val, wherein Xaal is any

amino acid and Xaa2 is any amino acid or is absent (SEQ ID NO:2). Preferably, the sequence is substantially identical to one of the BIR domain sequences provided for xiap, hiap-1, hiap-2 herein.

By "ring zinc finger" or "RZF" is meant a domain having the amino acid sequence of the consensus sequence: Glu-Xaal-Xaal-Xaal-Xaal-Xaal-Xaal-Xaa2-Xaal-Xaal-Xaal-Cys- Lys-Xaa3-Cys-Met-Xaal-Xaal-Xaal-Xaal-Xaal-Xaa3-Xaal-Phe-Xaal-Pro-Cys-Gly-His-Xaal-Xaal-Xaal-Cys-Xaal-Xaal-Cys-Ala- Xaal-Xaal-Xaal-Xaal-Xaal-Cys-Pro-Xaal-Cys, wherein Xaal is any amino acid, Xaa2 is Glu or Asp, and Xaa3 is Val or Ile (SEQ ID NO:l).

Preferably, the sequence is substantially identical to the RZF domains provided herein for the human or murine Xiap, Hiap-1, or Hiap-2.

By "enhancing apoptosis" is meant increasing the number of cells which apoptose in a given cell population. Preferably, the cell population is selected from a group including ovarian cancer cells, breast cancer cells, pancreatic cancer cells, T cells, neuronal cells, fibroblasts, or any other cell line known to proliferate in a laboratory setting. It will be appreciated that the degree of apoptosis enhancement provided by an apoptosis enhancing compound in a given assay will vary, but that one skilled in the art can determine the statistically significant change in the level of apoptosis which identifies a compound which enhances apoptosis otherwise limited by an IAP. Preferably, "enhancing apoptosis" means that the increase in the number of cells undergoing apoptosis is at least 25%, more preferably the increase is 50%, and most preferably the increase is at least one-fold. Preferably, the sample monitored is a sample of cells which normally undergo insufficient apoptosis (i.e., cancer cells).

By "proliferative disease" is meant a disease which is caused by or results in inappropriately high levels of cell division, inappropriately low levels of apoptosis, or both. For example, cancers such as lymphoma, leukemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, and lung cancer are all examples of proliferative disease.

By "polypeptide" is meant any chain of more than two amino acids, regardless of post-translational modification such as glycosylation or phosphorylation.

By "IAP or NAIP biological activity" is meant any activity known to be caused *in vivo* or *in vitro* by a NAIP or IAP polypeptide.

By "substantially identical" is meant a polypeptide or nucleic acid exhibiting at least 50%, preferably 85%, more preferably 90%, and most preferably 95% homology to a reference amino acid or nucleic acid sequence. For polypeptides, the length of comparison sequences will generally be at least 16 amino acids, preferably at least 20 amino acids, more preferably at least 25 amino acids, and most preferably 35 amino acids. For nucleic acids, the length of comparison sequences will generally be at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably 110 nucleotides.

Sequence identity is typically measured using sequence analysis software with the default parameters specified therein (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705). This software program matches similar sequences by assigning degrees of homology to various substitutions, deletions, and other modifications. Conservative

substitutions typically include substitutions within the following groups: glycine, alanine, valine, isoleucine, leucine; aspartic acid, glutamic acid, asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine.

By "substantially pure polypeptide" is meant a polypeptide that has been separated from the components that naturally accompany it. Typically, the polypeptide is substantially pure when it is at least 60%, by weight, free from the proteins and naturally-occurring organic molecules with which it is naturally associated. Preferably, the polypeptide is an IAP polypeptide that is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight, pure. A substantially pure IAP polypeptide may be obtained, for example, by extraction from a natural source (e.g., a fibroblast, neuronal cell, or lymphocyte) by expression of a recombinant nucleic acid encoding an IAP polypeptide, or by chemically synthesizing the protein. Purity can be measured by any appropriate method, e.g., by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

A protein is substantially free of naturally associated components when it is separated from those contaminants which accompany it in its natural state. Thus, a protein which is chemically synthesized or produced in a cellular system different from the cell from which it naturally originates will be substantially free from its naturally associated components. Accordingly, substantially pure polypeptides include those derived from eukaryotic organisms but synthesized in *E. coli* or other prokaryotes.

By "substantially pure DNA" is meant DNA that is free of the genes which, in the naturally-occurring genome of the organism from which the DNA of the invention is derived, flank the gene. The term therefore includes, for example,

a recombinant DNA which is incorporated into a vector; into an autonomously replicating plasmid or virus; or into the genomic DNA of a prokaryote or eukaryote; or which exists as a separate molecule (e.g., a cDNA or a genomic or cDNA fragment produced by PCR or restriction endonuclease digestion) independent of other sequences. It also includes a recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequence.

By "transformed cell" is meant a cell into which (or into an ancestor of which) has been introduced, by means of recombinant DNA techniques, a DNA molecule encoding (as used herein) an IAP polypeptide.

By "transgene" is meant any piece of DNA which is inserted by artifice into a cell, and becomes part of the genome of the organism which develops from that cell. Such a transgene may include a gene which is partly or entirely heterologous (i.e., foreign) to the transgenic organism, or may represent a gene homologous to an endogenous gene of the organism.

By "transgenic" is meant any cell which includes a DNA sequence which is inserted by artifice into a cell and becomes part of the genome of the organism which develops from that cell. As used herein, the transgenic organisms are generally transgenic mammalian (e.g., rodents such as rats or mice) and the DNA (transgene) is inserted by artifice into the nuclear genome.

By "transformation" is meant any method for introducing foreign molecules into a cell. Lipofection, calcium phosphate precipitation, retroviral delivery, electroporation, and biolistic transformation are just a few of the teachings which may be used. For example, biolistic transformation is a method for introducing foreign molecules into a cell using velocity driven microprojectiles such as tungsten or gold particles. Such velocity-driven methods originate from

pressure bursts which include, but are not limited to, helium-driven, air-driven, and gunpowder-driven techniques. Biolistic transformation may be applied to the transformation or transfection of a wide variety of cell types and intact tissues including, without limitation, intracellular organelles (e.g., and mitochondria and chloroplasts), bacteria, yeast, fungi, algae, animal tissue, and cultured cells.

By "positioned for expression" is meant that the DNA molecule is positioned adjacent to a DNA sequence which directs transcription and translation of the sequence (i.e., facilitates the production of, e.g., an IAP polypeptide, a recombinant protein or a RNA molecule).

By "reporter gene" is meant a gene whose expression may be assayed; such genes include, without limitation, glucuronidase (GUS), luciferase, chloramphenicol transacetylase (CAT), and β-galactosidase.

By "promoter" is meant minimal sequence sufficient to direct transcription. Also included in the invention are those promoter elements which are sufficient to render promoter-dependent gene expression controllable for cell type-specific, tissue-specific or inducible by external signals or agents; such elements may be located in the 5' or 3' regions of the native gene.

By "operably linked" is meant that a gene and one or more regulatory sequences are connected in such a way as to permit gene expression when the appropriate molecules (e.g., transcriptional activator proteins are bound to the regulatory sequences).

By "conserved region" is meant any stretch of six or more contiguous amino acids exhibiting at least 30%, preferably 50%, and most preferably 70% amino acid sequence identity between two or more of the IAP family members, (e.g., between human HIAP-1, HIAP-2, and XIAP). Examples of preferred

conserved regions are shown (as boxed or designated sequences) in Figures 5-7 and Tables 1 and 2, and include, without limitation, BIR domains and ring zinc finger domains.

By "detectably-labelled" is meant any means for marking and identifying the presence of a molecule, e.g., an oligonucleotide probe or primer, a gene or fragment thereof, or a cDNA molecule. Methods for detectably-labelling a molecule are well known in the art and include, without limitation, radioactive labelling (e.g., with an isotope such as ^{32}P or ^{35}S) and nonradioactive labelling (e.g., chemiluminescent labelling, e.g., fluorescein labelling).

By "antisense," as used herein in reference to nucleic acids, is meant a nucleic acid sequence, regardless of length, that is complementary to the coding strand of an IAP or NAIP gene. Preferably, the antisense nucleic acid is capable of enhancing apoptosis when present in a cell which normally does not undergo sufficient apoptosis. Preferably, the increase is at least 10%, relative to a control, more preferably 25%, and most preferably 1-fold or more.

By "purified antibody" is meant antibody which is at least 60%, by weight, free from proteins and naturally occurring organic molecules with which it is naturally associated. Preferably, the preparation is at least 75%, more preferably 90%, and most preferably at least 99%, by weight, antibody, e.g., an IAP specific antibody. A purified antibody may be obtained, for example, by affinity chromatography using recombinantly-produced protein or conserved motif peptides and standard techniques.

By "specifically binds" is meant an antibody that recognizes and binds a protein but that does not substantially recognize and bind other molecules in a sample, e.g., a biological sample, that naturally includes protein.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

Brief Description of the Drawings

Fig. 1 is the human xiap cDNA sequence (SEQ ID NO:3) and the XIAP polypeptide sequence (SEQ ID NO:4).

Fig. 2 is the human hiap-1 cDNA sequence (SEQ ID NO:5) and the HIAP-1 polypeptide sequence (SEQ ID NO:6).

Fig. 3 is the human hiap-2 cDNA sequence (SEQ ID NO:7) and the HIAP-2 polypeptide sequence (SEQ ID NO:8). The sequence absent in the hiap-2-Δ variant is boxed.

Fig. 4 is the murine xiap (also referred to as "miap-3") cDNA sequence (SEQ ID NO:9) and encoded murine XIAP polypeptide sequence (SEQ ID NO:10).

Fig. 5 is the murine hiap-1 (also referred to as "miap-1") cDNA sequence (SEQ ID NO:39) and the encoded murine HIAP-1 polypeptide sequence (SEQ ID NO:40).

Fig. 6 is the murine hiap-2 (also referred to as "miap-2") cDNA sequence (SEQ ID NO:41) and the encoded murine HIAP-2 polypeptide (SEQ ID NO:42).

Fig. 7 is a photograph of a Northern blot illustrating human hiap-1 and hiap-2 mRNA expression in human tissues.

Fig. 8 is a photograph of a Northern blot illustrating human hiap-2 mRNA expression in human tissues.

Fig. 9 is a photograph of a Northern blot illustrating human xiap mRNA expression in human tissues.

Fig. 10A - 10D are graphs depicting suppression of apoptosis by XIAP, HIAP-1, HIAP-2, bcl-2, smn, and 6-myc.

Fig. 11 is a photograph of an agarose gel containing cDNA fragments that were amplified, with hiap-1-specific primers, from RNA obtained from Raji, Ramos, EB-3, Burkitt's lymphoma cells, and Jiyoye cells, and cells from normal placenta.

Fig. 12 is a photograph of a Western blot containing protein extracted from Jurkat and astrocytoma cells stained with an anti-XIAP antibody. The position and size of a series of marker proteins is indicated.

Fig. 13 is a photograph of a Western blot containing protein extracted from Jurkat cells following treatment as described in Example XII. The blot was stained with a rabbit polyclonal anti-XIAP antibody. Lane 1, negative control; lane 2, anti-Fas antibody; lane 3, anti-Fas antibody and cycloheximide; lane 4, TNF-α; lane 5, TNF-α and cycloheximide.

Fig. 14 is a photograph of a Western blot containing protein extracted from HeLa cells following exposure to anti-Fas antibodies. The blot was stained with a rabbit polyclonal anti-XIAP antibody. Lane 1, negative control; lane 2, cycloheximide; lane 3, anti-Fas antibody; lane 4, anti-Fas antibody and cycloheximide; lane 5, TNF-α; lane 6, TNF-α and cycloheximide.

Figs. 15A and 15B are photographs of Western blots stained with rabbit polyclonal anti-XIAP antibody. Protein was extracted from HeLa cells (Fig. 21A) and Jurkat cells (Fig. 21B) immediately, 1, 2, 3, 5, 10, and 22 hours after exposure to anti-Fas antibody.

Figs. 16A and 16B are photographs of Western blots stained with an anti-CPP32 antibody (Fig. 16A) or a rabbit polyclonal anti-XIAP antibody (Fig. 16B). Protein was extracted from Jurkat cells immediately, 3 hours, or 7 hours after exposure to an anti-Fas antibody. In addition to total protein, cytoplasmic and nuclear extracts are shown.

Fig. 17 is a photograph of a polyacrylamide gel following electrophoresis of the products of an *in vitro* XIAP cleavage assay.

Figs. 18 and 19 shows the increased level of HIAP-1 and HIAP-2 mRNA, respectively, in breast cancer cell lines having p53 mutations (lanes 5-7). The bottom portion of the figure shows the control.

Fig. 20 shows the influence of Taxol on DNA fragmentation in Cisplatin-sensitive (right) and resistant (left) human ovarian epithelial cancer cells.

Fig. 21 shows the influence of Cisplatin on DNA fragmentation in sensitive (right) and resistant (left) human ovarian epithelial cancer cells.

Fig. 22 shows the effects of Taxol on XIAP and Hiap-2 protein levels in Cisplatin sensitive (right) and resistant (left) human ovarian epithelial cancer cells.

Figs. 23A and 23B show the influence of Taxol and TGFβ on HIAP-2 mRNA levels in Cisplatin sensitive (right) and resistant (left) human epithelial cancer cells.

Figs. 24A and 24B show the effect of TGFβ on XIAP protein expression (Fig. 24A) and DNA fragmentation (Fig. 24B) in Cisplatin sensitive and resistant cells.

Detailed Description

Previously, we have provided a novel family of inhibitors of apoptosis, the IAPs, and an additional related anti-apoptotic protein, NAIP. Here we provide identification of cancer types in which dysregulation of the IAPs and NAIP is apparent. Our results are of paramount importance and provide diagnostics, prognostics, treatments, and drug screens aimed at the detection and effective treatment of cancer.

Cancer Screening

We initially studied IAP expression levels in a variety of normal tissues and cancer cell lines using commercially available northern blots. Elevated *xiap*, *hiap-1* and *hiap-2* mRNA was noted in a surprising number of cancer lines of diverse lineage, including colorectal cancer, lymphoma, leukemia, and melanoma cell lines. In contrast, *Bcl-2* mRNA was elevated in only a single cell line. Although this result reinforced the importance of the IAPs in cancer, the question remained as to whether the individual cancer cell lines on the blot were representative of the cancer type. As a result, we screened panels of cancer cell lines of particular tumor type by northern blot and quantitative RT-PCR analysis in order to ascertain the frequency of IAP dysregulation. The results are summarized as follows:

Burkitt's Lymphoma

We studied both the frequency and consequences of IAP upregulation in Burkitt's lymphoma. Elevated levels of *hiap-1* and *hiap-2* have been found in the vast majority of the Burkitt's cell lines examined. Furthermore,

those Burkitt's lines expressing low levels of hiap-1 are transcriptionally activated by Epstein-Barr virus (EBV) infection.

Breast Adenocarcinoma

A key observation was made in this survey, in which a correlation was observed between drug resistance, p53 status and hiap-1/2 expression. Four of the cell lines possessed wild-type p53, while three possessed documented p53 mutations that correlated with resistance to the anti-cancer drug adriamycin. Significantly, the three lines which were relatively more drug resistant also displayed elevated hiap-1 and hiap-2 mRNA levels. These results indicate that one of the ways that p53 controls apoptosis is through regulation of these genes.

Ovarian Carcinoma

mRNA in situ analysis suggest a role for NAIP in the developmental biology of the ovary. Overexpression of hiap-2 and xiap mRNA has also been documented in some ovarian cancer cell lines.

Pancreatic Cancer

Approximately 25% of the cell lines tested to date demonstrate hiap-1 and hiap-2 mRNA elevation.

Summary of Cancer Panels

To date, a significant fraction of cancer cell lines of each type examined display elevated IAP levels. Our results indicate that hiap-1 and hiap-2

tend to be the most frequently and dramatically upregulated. The apparent coordinate regulation of both genes was surprising given their very different normal tissue distribution. hiap-1 and hiap-2 reside in tandem array on chromosome 11q23, a site frequently rearranged in lymphomas and leukemias.

Transcriptional regulation of the IAPs in cancer cell lines

Our experiments have established a correlation between p53 status and transcriptional overexpression of hiap-1 and hiap-2. This provides an important new way in which to enhance apoptosis, particularly in view of the fact that the mechanism by which p53 controls cell fate remains largely unknown. It has previously been documented that wild-type p53 negatively down-regulates *Bcl-2*, and positively upregulates the Bcl-2 antagonist *Bax*. In some cancer cell types, mutation of p53 causes a two-fold effect; namely, the upregulation of Bcl-2, and down regulation of Bax, both of which contribute to the anti-apoptotic phenotype. While not wishing to bind ourselves to a particular theory, we believe that wild-type p53 also transcriptionally suppresses *hiap-1* and *hiap-2*. DNA damage that includes the increase in wild-type levels p53 levels would therefore result in decreased hiap-1 and hiap-2 in normal cells, resulting in apoptosis. Mutations in the p53 gene would therefore result in a loss of transcriptional control of these *iap* genes. As a result, p53 mutant cancer cells would display constitutively high levels of hiap-1 and hiap-2, rendering the cells resistant to anti-cancer therapies. The p53/hiap-1 and hiap-2 correlations may be extended to the other cancer cell line panels. One may directly demonstrate p53 regulation of the IAPs using transfection assays and northern blot analysis.

Accordingly, we predict that cancer cells having p53 mutations (p53*) will have increased IAP levels resulting in a poor response to chemotherapeutics. Because IAP levels may be assessed more readily than the presence of a p53* mutation, our discovery also provides an important improvement in cancer diagnosis and prognosis (see below).

Transgenic Mice

We have constructed a number of IAP and NAIP transgenic mouse expression vectors, including T-cell, B-cell, and neuronal specific promoter constructs. Founder mice have been identified, are viable, and for most of these constructs and we have developed breeding colonies. These mice will likely be prone to cancers of the tissue types in which the promoter is active. Thus the mice provide an excellent resource for testing the efficacy of anti-sense oligos and for screening for apoptosis enhancing cancer therapeutics. Standard mouse drug screening models and gene delivery protocols may be employed to utilize the mice for this purpose.

Diagnostic/Prognostic Reagents

There is a relative lack of diagnostic and prognostic tests which clinical oncologists may utilize in determining the appropriate degree of intervention in the treatment of cancer. Mutation of the p53 gene remains one of the best prognostic indicators in cancer biology. However, the number of different mutations identified to date is great and scattered throughout the gene. In addition, many mutations in p53 result in an inappropriate stabilization of the protein, which allows detection at the protein level rather than at the mRNA level.

Mutations which alter the transactivation/repression activities of the protein are not necessarily apparent at either the mRNA or protein levels. On the other hand, if IAP and NAIP expression levels correlate with p53 mutation they may provide more valuable prognostic information and assist in the determination of which patients require more aggressive treatment. Thus the invention provides two assays for prognosis an diagnosis. Semi-quantitative RT-PCR based assays may be used to assay for *iap* and/or *naip* gene or protein expression levels. Alternatively, monoclonal antibodies may be incorporated into an ELISA (enzyme linked immunosorbent assay) type assay for direct determination of protein levels.

Therapeutic Products

For IAP related therapies one may employ the paradigms utilized for Bcl-2 and RAS antisense development, although accommodation of IAP mutation is not required (in contrast to ras antisense). Most useful are antisense constructs which enhance apoptosis at least 10%, preferably by enhancing degradation of the RNA in the nucleus.

In addition to antisense approached described herein the invention features small molecule screening assays which may be used to identify lead compounds that negatively regulate the *iaps*. For example, compounds which enhance apoptosis in the presence of IAP overexpression or which decrease the level of IAP biological activity may be detected and are useful cancer therapeutics.

Molecules that are found, by the methods described above, to effectively modulate IAP gene expression or polypeptide activity may be tested further in animal models. If they continue to function successfully in an *in vivo*

setting, they may be used as therapeutics to either inhibit or enhance apoptosis, as appropriate.

Manipulation of cancer chemotherapeutic drug resistance using an antisense oligonucleotide and fragment approaches.

We have documented that overexpression of the IAPs renders cell lines resistant to serum growth factor withdrawal, tumor necrosis factor alpha (TNF) and menadione exposure, all of which are treatments that normally induce apoptosis. Herein we describe the extension of these studies to cancer cell lines using apoptotic triggers used in clinical situations, such as doxorubicin, adriamycin, and methotrexate. Our findings have led up to design antisense RNA therapeutics. Rapid screening of multiple cell lines for apoptotic response has been made feasible through the generation of a series of sense and antisense adenoviral IAP and NAIP expression vectors, as well as control lacZ viruses. One may now show enhanced drug resistance using the expression constructs. In addition, anti-sense adenovirus constructs may be developed and used to test reversal of the drug resistant phenotype of appropriate cell lines. We have surveyed cancer cell lines with the objective of identifying tumor types in which IAP overexpression is apparent or altered and these results are described both above and in the Examples below. Concomitant to this research, we have designed a series of antisense oligonucleotides to various regions of each of the *iaps*. These oligos may be used to enhance drug sensitivity after testing in an assay system, i.e., with the adenoviral vectors system. Animal modeling of the effectiveness of antisense IAP oligos may also be employed as a step in testing

and appropriate transgenic mammals for this are described above and also generally available in the art.

The following describes some of the testing systems which may be employed.

Anti-Cancer Gene Therapy

Retroviral vectors, adenoviral vectors, adeno-associated viral vectors, or other viral vectors with the appropriate tropism for cells likely requiring enhanced apoptosis (for example, breast cancer and ovarian cancer cells) may be used as a gene transfer delivery system for a therapeutic gene constructs. Numerous vectors useful for this purpose are generally known (Miller, Human Gene Therapy 15-14, 1990; Friedman, Science 244:1275-1281, 1989; Eglitis and Anderson, BioTechniques 6:608-614, 1988; Tolstoshev and Anderson, current opinion in Biotechnology 1:55-61, 1990; Sharp, The Lancet 337:1277-1278, 1991; Cornetta et al., Nucleic Acid Research and Molecular Biology 36:311-322, 1987; Anderson, Science 226:401-409, 1984; Moen, Blood Cells 17:407-416, 1991; Miller et al., BioTechniques 7:980-990, 1989; Le Gal La Salle et al., Science 259:988-990, 1993; and Johnson, Chest 107:77S-83S, 1995).

Retroviral vectors are particularly well developed and have been used in clinical settings (Rosenberg et al., N. Engl. J. Med 323:370, 1990; Anderson et al., U.S. Patent No. 5,399,346). Non-viral approaches may also be employed for the introduction of therapeutic DNA into cells otherwise predicted to undergo apoptosis. For example, IAP may be introduced into a neuron or a T cell by lipofection (Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413, 1987; Ono et al., Neurosci. Lett. 117:259, 1990; Brigham et al., Am. J. Med. Sci. 298:278, 1989;

Staubinger et al., Meth. Enz. 101:512, 1983), asialorosonucoid-polylysine conjugation (Wu et al., J. Biol. Chem. 263:14621, 1988; Wu et al., J. Biol. Chem. 264:16985, 1989); or, less preferably, microinjection under surgical conditions (Wolff et al., Science 247:1465, 1990).

For any of the methods of application described above, the therapeutic nucleic acid construct is preferably applied to the site of the needed apoptosis event (for example, by injection). However, it may also be applied to tissue in the vicinity of the predicted apoptosis event or to a blood vessel supplying the cells predicted to require enhanced apoptosis.

In the constructs described, nucleic acid expression can be directed from any suitable promoter (e.g., the human cytomegalovirus (CMV), simian virus 40 (SV40), or metallothionein promoters), and regulated by any appropriate mammalian regulatory element. For example, if desired, enhancers known to preferentially direct gene expression in ovarian cells, breast tissue, neural cells, T cells, or B cells may be used to direct expression. The enhancers used could include, without limitation, those that are characterized as tissue- or cell-specific in their expression. Alternatively, if a clone used as a therapeutic construct, regulation may be mediated by the cognate regulatory sequences or, if desired, by regulatory sequences derived from a heterologous source, including any of the promoters or regulatory elements described above.

Less preferably, anti-cancer gene therapy is accomplished by direct administration of the therapeutic mRNA or antisense IAP mRNA to a cell that is expected to require enhanced apoptosis. The mRNA may be produced and isolated by any standard technique, but is most readily produced by *in vitro* transcription using an IAP related nucleic acids under the control of a high

efficiency promoter (e.g., the T7 promoter). Administration of IAP antisense mRNA to malignant cells can be carried out by any of the methods for direct nucleic acid administration described above.

Ideally, the production of IAP protein by any gene therapy approach will result in cellular levels of and/or fragments thereof that are at least equivalent to the normal, cellular level of IAP in an unaffected cell. Treatment by any IAP-modulating gene therapy approach may be combined with more traditional therapies.

Another therapeutic approach within the invention involves administration of recombinant IAP protein fragments or IAP antibodies, either directly to the site where enhanced apoptosis is desirable (for example, by injection) or systemically (for example, by any conventional recombinant protein administration technique).

The dosage of IAP, the IAP fragment, IAP mutant protein or IAP antibody depends on a number of factors, including the size and health of the individual patient, but, generally, between O.l mg and 100 mg inclusive are administered per day to an adult in any pharmaceutically acceptable formulation.

Administration

An IAP mutant protein or protein fragment, gene encoding the same, gene encoding IAP antisense RNA, or modulator of an IAPs may be administered within a pharmaceutically-acceptable diluent, carrier, or excipient, in unit dosage form. Conventional pharmaceutical practice may be employed to provide suitable formulations or compositions to administer the compounds to patients suffering from a disease that is caused by excessive cell proliferation. Administration may

begin before the patient is symptomatic. Any appropriate route of administration may be employed, for example, administration may be parenteral, intravenous, intraarterial, subcutaneous, intramuscular, intracranial, intraorbital, ophthalmic, intraventricular, intracapsular, intraspinal, intracisternal, intraperitoneal, intranasal, aerosol, suppository, or oral administration. For example, therapeutic formulations may be in the form of liquid solutions or suspensions; for oral administration, formulations may be in the form of tablets or capsules; and for intranasal formulations, in the form of powders, nasal drops, or aerosols.

Methods well known in the art for making formulations are found, for example, in "Remington's Pharmaceutical Sciences." Formulations for parenteral administration may, for example, contain excipients, sterile water, or saline, polyalkylene glycols such as polyethylene glycol, oils of vegetable origin, or hydrogenated napthalenes. Biocompatible, biodegradable lactide polymer, lactide/glycolide copolymer, or polyoxyethylene-polyoxypropylene copolymers may be used to control the release of the compounds. Other potentially useful parenteral delivery systems for IAP modulatory compounds include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. Formulations for inhalation may contain excipients, for example, lactose, or may be aqueous solutions containing, for example, polyoxyethylene-9-lauryl ether, glycocholate and deoxycholate, or may be oily solutions for administration in the form of nasal drops, or as a gel.

If desired, treatment with an IAP mutant proteins or IAP fragments, related genes, or other modulatory compounds may be combined with more traditional therapies for the proliferative disease such as surgery or chemotherapy.

Detection of Conditions Involving Insufficient Apoptosis

IAP polypeptides and nucleic acid sequences find diagnostic use in the detection or monitoring of conditions involving insufficient levels of apoptosis, i.e., proliferative disease. For example, increased expression of IAPs, altercations in localization, and IAP cleavage correlate with inhibition of apoptosis and cancer in humans. Accordingly, an increase in the level of IAP production may provide an indication of a proliferative condition or a predisposition to such a condition. Levels of IAP expression may be assayed by any standard technique. For example, IAP expression in a biological sample (e.g., a biopsy sample) may be monitored by standard Northern blot analysis or may be aided by PCR (see, e.g., Ausubel et al., *supra*; PCR Technology: Principles and Applications for DNA Amplification, H.A. Ehrlich, Ed. Stockton Press, NY; Yap et al. Nucl. Acids. Res. 19:4294, 1991).

Alternatively, a biological sample obtained from a patient may be analyzed for one or more mutations in the IAP sequences or p53 sequences using a mismatch detection approach. Generally, these techniques involve PCR amplification of nucleic acid from the patient sample, followed by identification of the mutation (i.e., mismatch) by either altered hybridization, aberrant electrophoretic gel migration, binding or cleavage mediated by mismatch binding proteins, or direct nucleic acid sequencing. Any of these techniques may be used to facilitate mutant IAP detection, and each is well known in the art; examples of particular techniques are described, without limitation, in Orita et al., Proc. Natl. Acad. Sci. USA 86:2766-2770, 1989; Sheffield et al., Proc. Natl. Acad. Sci. USA 86:232-236, 1989).

In yet another approach, immunoassays are used to detect or monitor IAP protein in a biological sample. IAP-specific polyclonal or monoclonal antibodies (produced as described above) may be used in any standard immunoassay format (e.g., ELISA, Western blot, or RIA) to measure IAP polypeptide level or IAP levels from cancerous control cells. These levels would be compared to wild-type IAP levels, with a decrease in IAP production relative to a wild-type cell indicating a condition involving increased apoptosis and a decrease relative to a known cancer cell indicating a decreased likelihood of an IAP related cancer. Examples of immunoassays are described, e.g., in Ausubel et al., *supra*. Immunohistochemical techniques may also be utilized for IAP detection. For example, a tissue sample may be obtained from a patient, sectioned, and stained for the presence of IAP using an anti-IAP antibody and any standard detection system (e.g., one which includes a secondary antibody conjugated to horseradish peroxidase). General guidance regarding such techniques can be found in, e.g., Bancroft and Stevens (Theory and Practice of Histological Techniques, Churchill Livingstone, 1982) and Ausubel et al. (*supra*).

In one preferred example, a combined diagnostic method may be employed that begins with an evaluation of IAP protein production (for example, by immunological techniques or the protein truncation test (Hogerrorst et al., Nature Genetics 10:208-212, 1995)) and also includes a nucleic acid-based detection technique designed to identify more subtle IAP altercations, e.g., mutations. As described above, a number of mismatch detection assays are available to those skilled in the art, and any preferred technique may be used. Mutations in IAP may be detected that either result in enhanced IAP expression or altercations in IAP biological activity. In a variation of this combined diagnostic

method, IAP biological activity is measured as anti-apoptotic activity using any appropriate apoptosis assay system (for example, those described above).

Mismatch detection assays also provide an opportunity to diagnose an IAP-mediated predisposition to diseases caused by insufficient apoptosis. For example, a patient heterozygous for an IAP mutation may show no clinical symptoms and yet possess a higher than normal probability of developing one or more types of proliferative diseases. Given this diagnosis, a patient may take precautions to minimize their exposure to adverse environmental factors (for example, UV exposure or chemical mutagens) and to carefully monitor their medical condition (for example, through frequent physical examinations). This type of IAP diagnostic approach may also be used to detect IAP mutations in prenatal screens. The IAP diagnostic assays described above may be carried out using any biological sample (for example, any biopsy sample or bodily fluid or tissue) in which IAP is normally expressed. Identification of a mutant IAP gene may also be assayed using these sources for test samples.

Alternatively, an altercation in IAP activity, particularly as part of a diagnosis for predisposition to IAP-associated proliferative disease, may be tested using a nucleic acid sample from any cell, for example, by mismatch detection techniques. Preferably, the DNA sample is subjected to PCR amplification prior to analysis.

Example 1: Elevated IAP Levels in Cancer Cell Lines

In order to specifically demonstrate the utility of IAP gene sequences as diagnostics and prognostics for cancer, a Human Cancer Cell Line Multiple Tissue Northern Blot (Clontech, Palo Alto, CA; #7757-1) was probed. This

Northern blot contained approximately 2 μg of poly A^+ RNA per lane from eight different human cell lines: (1) promyelocytic leukemia HL-60, (2) HeLa cell S3, (3) chronic myelogenous leukemia K-562, (4) lymphoblastic leukemia MOLT-4, (5) Burkitt's lymphoma Raji, (6) colorectal adenocarcinoma SW480, (7) lung carcinoma A549, and (8) melanoma G361. As a control, a Human Multiple Tissue Northern Blot (Clontech, Palo Alto, CA; #7759-1) was probed. This Northern blot contained approximately 2 μg of poly A^+ RNA from eight different human tissues: (1) spleen, (2) thymus, (3) prostate, (4) testis, (5) ovary, (6) small intestine, (7) colon, and (8) peripheral blood leukocytes.

The Northern blots were hybridized sequentially with: (1) a 1.6 kb probe to the xiap coding region, (2) a 375 bp hiap-2 specific probe corresponding to the 3' untranslated region, (3) a 1.3 kb probe to the coding region of hiap-1, which cross-reacts with hiap-2, (4) a 1.0 kb probe derived from the coding region of bcl-2, and (5) a probe to β-actin, which was provided by the manufacturer. Hybridization was carried out at 50°C overnight, according to the manufacturer's suggestion. The blot was washed twice with 2X SSC, 0.1% SDS at room temperature for 15 minutes and then with 2X SSC, 0.1% SDS at 50°C.

All cancer lines tested showed increased IAP expression relative to samples from non-cancerous control tissues (Table 1). Expression of xiap was particularly high in HeLa (S-3), chronic myelogenous leukemia (K-562), colorectal adenocarcinoma (SW-480), and melanoma (G-361) lines. Expression of hiap-1 was extremely high in Burkitt's lymphoma, and was also elevated in colorectal adenocarcinoma. Expression of hiap-2 was particularly high in chronic myelogenous leukemia (K-562) and colorectal adenocarcinoma (SW-480). Expression of Bcl-2 was upregulated only in HL-60 leukemia cells.

TABLE 1

NORTHERN BLOT IAP RNA LEVELS IN CANCER CELLS*

	xiap	hiap1	hiap2
Promyelocytic Leukemia HL-60	+	+	+
HeLa S-3	+	+	+
Chronic Myelogenous Leukemia K-562	+++	+	+++
Lymphoblastic Leukemia MOLT-4	+++	+	+
Burkitt's Lymphoma Raji	+	+(x10)	+
Colorectal Adenocarcinoma SW-480	+++	+++	+++
Lung Carcinoma A-549	+	+	+
Melanoma G-361	+++	+	+

*Levels are indicated by a (+) and are the approximate increase in RNA levels relative to Northern blots of RNA from non-cancerous control cell lines. A single plus indicates an estimated increase of at least 1-fold

These observations indicate that upregulation of the anti-apoptotic IAP genes may be a widespread phenomenon in proliferative diseases, perhaps occurring much more frequently than upregulation of Bcl-2. Furthermore, upregulation may be necessary for the establishment or maintenance of the transformed state of cancerous cells.

In order to pursue the observation described above, i.e., that hiap-1 is overexpressed in the Raji Burkitt's lymphoma cell line, RT-PCR analysis was performed in multiple Burkitt's lymphoma cell lines. Total RNA was extracted

from cells of the Raji, Ramos, EB-3, and Jiyoye cell lines, and as a positive control, from normal placental tissue. The RNA was reverse transcribed, and amplified by PCR with the following set of oligonucleotide primers: 5'-AGTGCGGGTTTTTATTATGTG-3' (SEQ ID NO:15) and 5'-AGATGACCACAAGGAATAAACACTA-3' (SEQ ID NO:16), which selectively amplify a hiap-1 cDNA fragment. RT-PCR was conducted using a Perkin Elmer 480 Thermocycler to carry out 35 cycles of the following program: 94°C for 1 minute, 50°C for 1.5 minutes, and 72°C for a minute. The PCR reaction product was electrophoresed on an agarose gel and stained with ethidium bromide. Amplified cDNA fragments of the appropriate size were clearly visible in all lanes containing Burkitt's lymphoma samples, but absent in the lanes containing the normal placental tissue sample, and absent in lanes containing negative control samples, where template DNA was omitted from the reaction (Fig. 11).

Example 2: IAPs in Breast Cancer

The following data relate to the regulation and role of HIAPs in cancer cells. Figs 18 and 19 show data demonstrating that HIAP-1 and HIAP-2 are both upregulated in breast cancer cell lines that contain mutant p53. The lanes contain 20 μg of total RNA from the following lines: 1. MCF-7(clone 1, wt p53) 2. MCF-7 (clone 2, wt p53) 3. MCF-7 (American Type Culture Collection, wt p53) 4. MCF-7 (parental line, California, wt p53) 5. MCF-7 (California, adriamycin resistant variant, mutant p53) , 6. MDA MB 231 (ATCC, mutant p53, codon 280) 7.T47-D (ATCC, mutant p53, codon 194) 7. ZR-75 (ATCC, wt p53).

The amount of RNA loaded on each gel was controlled for by hybridization with glycerol phosphate dehydrogenase (GAPDH).

Example 3: IAPs in Ovarian Cancer

Overview

Epithelial ovarian cancer is the leading cause of death from gynecologic malignancy. Although clinical and histologic prognostic factors such as tumor grade and surgical stage are well understood, the biologic process that leads to uncontrolled cellular growth is less clear. The control of cell numbers during tissue growth is thought to be the results of a balance of cell proliferation and cell death. An aberration in this natural homeostasis likely contributes to malignant cellular transformation.

Recent studies on ovarian cancer cell biology have suggested that the deregulation of apoptosis may be one of the underlying pathologic mechanism in this disease. However, the molecular mechanisms involved in its regulation is poorly understood and the role and regulation of the IAP genes in ovarian cell transformation have not been examined previously. Ovarian epithelial cancer is in part a result of suppressed apoptosis of ovarian surface epithelial cells. The effectiveness of certain chemotherapeutic agents rests on their ability to induce cell death. The loss of responsiveness of the cells to these agents is due to a desensitization of the apoptotic process to these agents. The regulation of ovarian epithelial cell apoptosis involves changes in the expression of IAP genes and post-translational modification/processing of the IAP gene products.

We have conducted experiments and now believe that IAPs play a key role in maintaining the normal growth of ovarian surface epithelial cells and

that the overexpression of these genes leads to cellular transformation. Furthermore, we have discovered that the effectiveness of chemotherapeutic agents in the treatment of this form of malignancy rests upon their ability to suppress the expression of the IAP genes. By seeking to control the regulation of the IAP genes in human ovarian epithelial cancer cells we have provided a rational approach for the development of new chemotherapeutics for patients both responsive and resistant to current cancer drugs. Similarly, assays designed to detect compounds which decrease IAP biological activity provide a rational method for drug discovery.

Methods

A) Human Ovarian Epithelial Cancer Cell Culture

Cisplatin-sensitive (OV2008) and -resistant (C13) human ovarian epithelial cells were cultured in a chemically-defined medium at 37°C for up to 48 hours in the presence or absence of TGFβ (20 ng/ml), taxol (0 - 1.0 μM) or cisplatin (0 - 30 μM). At the end of the culture period, cells were either fixed for immunocytochemistry and TUNEL analyses, or snap frozen for subsequent extraction for IAP mRNA and proteins analyses.

B) Identification of Cell Death

Nuclear Staining:

Human ovarian epithelial cancer cells were fixed (4% formalin in PBS; 10 min. RT), washed in PBS, resuspended in Hoescht 33248 stain (0.1 μg/ml PBS, 10 min) washed again and spotted onto slides for microscopy. Nuclear staining was observed and photographed using a Zeiss fluorescent microscope

equipped with an FITC filter. Apoptotic cells were identified by typical nuclear morphology, and counted using randomly selected fields and numbered photographic slides to avoid bias during counting.

Quantification of DNA Ladders:

Cellular DNA was extracted using the Qiagen Blood Amt kit. DNA was quantified by ethidium bromide fluorescence. DNA (0.5 μg) was then end labelled by incubating (20 min, RT) with Klenow enzyme (2 U in 10 mM Tris + 5 mM $MgCl_2$) and 0.1 μCi [α32P]dCTP. Unincorporated nucleotides were removed with the Qiagen nucleotide removal kit and samples were resolved by Tris-acetate-EDTA agarose (1.8%) gel electrophoresis. The gel was then dried (2 hr, no heat) and exposed to a Bio-Rad phosphoimager screen to densitometrically quantify low molecular weight DNA (<15 kBp) and subsequently to x-ray film at -80°C.

In Situ TUNEL Labelling of Apoptotic Cells:

To identify cell death using the in situ cell death detection kit (Boehringer-Mannheim), slides prepared for histology were treated (20 min. 37°C) with terminal tranferase in the presence of FITC-conjugated dUTP.

C) Western Blot Analyses for IAPs

Protein extracts were prepared from human surface epithelial cancer cells sonicated (8s/cycle, 3 cycles) on ice in sucrose buffer (0.25 M sucrose, 0.025 M NaCl, 1 mM EGTA and 15 mM Tris-HCl pH 6.8, supplemented with 1 mM PMSF, 2 μg/ml of leupeptin and 5 μg/ml of aprotinin. The sonicates were centrifuged at 13,000xg for 10 min, the supernatants were collected and stored at -

20°C until electrophoretic analyses were performed. Protein concentration was determined by Bio-Rad Protein Assay. Proteins (10-30 μg) were resolved by one-dimensional SDS-PAGE, and electrophoretically transferred to nitrocellulose membrane. Membranes were blocked with 5% non-fat milk, and subsequently incubated with rabbit polyclonal antibody for IAP [anti-human Hiap-2ΔE(960529; 1:1000 dilution), anti-human NAIP E1.0 (951015; 1:1000 dilution) or anti-human Xiap (1:1000 dilution) diluted in TBST (10 mM Tris-buffered saline, 0.1% Tween-20, pH 7.5) containing 5% milk. An ECL kit was used to visualize immunopositive protein.

D) Northern Blots for IAP mRNAs

Total RNA from ovarian surface epithelial cancer cells by using RNeasy Kit (Qiagen). The RNA samples (10-15 μg) were quantified spectrophotometrically and size-fractioned by electrophoresis on formaldehyde-agarose gels (1.1%) containing 1 μg/ml ethidium bromide to confirm even loading of RNA samples and adequate separation of 28S and 18S ribosomal bands. The RNAs bands were blotted onto a nylon membrane and cross-linked by UV light. Membranes were prehybridized in 50% formamide, saline sodium citrate (SSC; 750 mM NaCl, 75 mM Na citrate), 1X Denhardt's solution, 1% SDS, 4 mM EDTA and 100 μg/ml sheared salmon sperm DNA for 4 h at 42°C. Hybridization was performed overnight at 42 °C with 20 million cpm of ^{32}P-labelled IAP cDNA probes (rat Naip, rat Xiap or human Hiap-2) added to the prehybridization buffer. The membranes were then washed twice with SSC (300 mM NaCl, 30 mM Na citrate) in 0.1% SDS for 20 min at room temperature and twice with SSC (30 mM NaCl, 3 mM sodium citrate) in 0.1% SDS for 20 min at 55°C and exposed to X-

ray film at -80°C for visualization. Densitometric analysis of various IAPs and 28S rRNA band was performed with the Image Analysis Systems from Bio-Rad Laboratories. Data were normalized by the respective 28S and expressed as a percentage of the control (defined as 100%).

Results

Cisplatin induced a concentration-dependent increase in the incidence of apoptosis in cisplatin-sensitive (OV2008) but to a lesser extent in -resistant (C13) human ovarian epithelial cells in vitro (Fig. 20). Similarly, Taxol also induced apoptosis in OV2008 cells, but to a lesser extent in the C13 cells (Fig. 21).

Basal XIAP and HIAP-2 protein contents were markedly higher in cisplatin-sensitive than -resistant cells. Taxol (0.04-1.0 μM) decreased XIAP and HIAP-2 protein levels in a concentration-dependent manner, the response being more pronounced in sensitive than resistant cells (Fig. 22). A lower molecular weight (approx. 45 kDa) immunoreactive fragment of HIAP-2 was also evident in both the sensitive and resistant cells. The content of this fragment was increased in the C13 cells but decreased in OV2008 cells by Taxol (Fig. 22).

Whereas Taxol (0.2 μM) marked suppressed HIAP-2 mRNA abundance in cisplatin-sensitive cells (approx. 80%), it was ineffective in the resistant cells (Fig. 23).

TGFβ (20 ng/ml) induced apoptosis in OV2008 but not in C13. Although its influence on Xiap protein content in cisplatin-resistant cells was only marginal, it markedly suppressed the protein level of this IAP in the cisplatin-

sensitive cells (Fig. 24A, 24B). TGFβ (20 ng/ml) also decreased HIAP-2 mRNA in OV2008 but not C13 cells (Fig. 23).

Significant observations and possible applications

Induction of apoptosis in human ovarian epithelial cancer cell by taxol was accompanied by suppressed IAP gene expression. The lost of sensitivity of the cells to the chemotherapeutic agent may be associated with its decreased ability to express these genes and to induce apoptosis. In drug-resistant cells, the decreased Hiap-2 protein content (in the face of an absence of noticeable change in Hiap-2 mRNA abundance) in the presence of Taxol was accompanied an increase in the intensity of a 45 kDa immunoreactive HIAP-2 protein band. These observations lead us to believe that the 45 kDa protein is a proteolytic product of HIAP-2 and plays a role in the development of drug resistance. In addition, the sensitivity of the IAP family in these ovarian cancer cells to Taxol suggest possible novel sites for gene targeting in the development of new chemotherapeutic agents for the treatment of human ovarian epithelial cell cancer.

<u>Example 4: Accumulation of a 26 kDa Cleavage Protein in Astrocytoma Cells</u>

Identification of a 26 kDa Cleavage Protein

A total protein extract was prepared from Jurkat and astrocytoma cells by sonicating them (X3 for 15 seconds at 4°C) in 50 mM Tris-HCl (pH 8.0), 150 mM NaCl, 1 mM PMSF, 1 μg/ml aprotinin, and 5 mM benzamidine. Following sonication, the samples were centrifuged (14,000 RPM in a microfuge) for five minutes. Twenty μg of protein was loaded per well on a 10% SDS-polyacrylamide gel, electrophoresed, and electroblotted by standard methods to

PVDF membranes. Western blot analysis, performed as described previously, revealed that the astrocytoma cell line (CCF-STTG1) abundantly expressed an anti-xiap reactive band of approximately 26 kDa, despite the lack of an apoptotic trigger event (Fig. 12). In fact, this cell line has been previously characterized as being particularly resistant to standard apoptotic triggers.

A 26 kDa xiap-reactive band was also observed under the following experimental conditions. Jurkat cells (a transformed human T cell line) were induced to undergo apoptosis by exposure to an anti-Fas antibody (1 μg/ml). Identical cultures of Jurkat cells were exposed either to: (1) anti-Fas antibody and cycloheximide (20 μg/ml), (2) tumor necrosis factor alpha (TNF-α, at 1,000 U/ml), or (3) TNF-α and cycloheximide (20 μg/ml). All cells were harvested 6 hours after treatment began. In addition, as a negative control, anti-Fas antibody was added to an extract after the cells were harvested. The cells were harvested in SDS sample buffer, electrophoresed on a 12.5% SDS polyacrylamide gel, and electroblotted onto PVDF membranes using standard methods. The membranes were immunostained with a rabbit polyclonal anti-xiap antibody at 1:1000 for 1 hour at room temperature. Following four 15 minute washes, a goat anti-rabbit antibody conjugated to horse-radish peroxidase was applied at room temperature for 1 hour. Unbound secondary antibody was washed away, and chemiluminescent detection of xiap protein was performed. The Western blot revealed the presence of the full-length, 55 kDa xiap protein, both in untreated and treated cells. In addition, a novel, approximately 26 kDa xiap-reactive band was also observed in apoptotic cell extracts, but not in the control, untreated cell extracts (Fig. 13).

Cleavage of xiap occurs in a variety of cell types, including other cancer cell lines such as HeLa. The expression of the 26 kDa xiap cleavage product was demonstrated in HeLa cells as follows. HeLa cells were treated with either: (1) cyclohexamide (20 μg/ml), (2) anti-Fas antibody (1 μg/ml), (3) anti-Fas antibody (1 μg/ml) and cyclohexamide (20 μg/ml), (4) TNFα (1,000 U/ml), or (5) TNFα (1,000 U/ml) and cyclohexamide (20 μg/ml). All cells were harvested 18 hours after treatment began. As above, anti-Fas antibody was added to an extract after the cells were harvested. HeLa cells were harvested, and the Western blot was probed under the same conditions as used to visualize xiap-reactive bands from Jurkat cell samples. A 26 kDa xiap band was again seen in the apoptotic cell preparations (Fig. 14). Furthermore, the degree of xiap cleavage correlated positively with cellular exposure to apoptotic triggers. Treatment of HeLa cells with cycloheximide or TNFα alone caused only minor apoptosis, and little cleavage product was observed. If the cells were treated with the anti-Fas antibody, a greater amount of cleavage product was apparent. These data indicate that xiap is cleaved in more than one cell type and in response to more than one type of apoptotic trigger.

Time Course of Expression

The time course over which the 26 kDa cleavage product accumulates was examined by treating HeLa and Jurkat cells with anti-Fas antibody (1 μg/ml) and harvesting them either immediately, or 1, 2, 3, 5, 10, or 22 hours after treatment. Protein extracts were prepared and Western blot analysis was performed as described above. Both types of cells accumulated increasing

quantities of the 26 kDa cleavage product over the time course examined (Figs. 15A and 15B).

Subcellular Localization of the 26 kDa xiap Cleavage Product

In order to determine the subcellular location of the 26 kDa cleavage product, Jurkat cells were induced to undergo apoptosis by exposure to anti-Fas antibody (1 μg/ml) and were then harvested either immediately, 3 hours, or 7 hours later. Total protein extracts were prepared, as described above, from cells harvested at each time point. In order to prepare nuclear and cytoplasmic cell extracts, apoptotic Jurkat cells were washed with isotonic Tris buffered saline (pH 7.0) and lysed by freezing and thawing five times in cell extraction buffer (50 mM PIPES, 50 mM KCl, 5 mM EGTA, 2 mM $MgCl_2$, 1 mM DTT, and 20 μM cytochalasin B). Nuclei were pelleted by centrifugation and resuspended in isotonic Tris (pH 7.0) and frozen at -80°C. The cytoplasmic fraction of the extract was processed further by centrifugation at 60,000 RPM in a TA 100.3 rotor for 30 minutes. Supernatants were removed and frozen at -80°C. Samples of both nuclear and cytoplasmic fractions were loaded on a 12.5% SDS-polyacrylamide gel, and electroblotted onto PVDF membranes. Western blot analysis was then performed using either an anti-CPP32 antibody (Transduction Laboratories Lexington, KY; Fig. 16A) or the rabbit anti-XIAP antibody described above (Fig. 16B).

The anti-CPP32 antibody, which recognizes the CPP32 protease (also known as YAMA or Apopain) partitioned almost exclusively in the cytoplasmic fraction. The 55 kDa XIAP protein localized exclusively in the cytoplasm of apoptotic cells, in agreement with the studies presented above, where XIAP protein in normal, healthy COS cells was seen to localize, by immunofluoresence

microscopy, to the cytoplasm. In contrast, the 26 kDa cleavage product localized exclusively to the nuclear fraction of apoptotic Jurkat cells. Taken together, these observations suggest that the anti-apoptotic component of XIAP could be the 26 kDa cleavage product, which exerts its influence within the nucleus.

In vitro Cleavage of xiap protein and Characterization of the Cleavage Product

For this series of experiments, xiap protein was labeled with ^{35}S using the plasmid pcDNA3-6myc-XIAP, T7 RNA polymerase, and a coupled transcription/translation kit (Promega) according to the manufacturer's instructions. Radioactively labeled xiap protein was separated from unincorporated methionine by column chromatography using Sephadex G-50™. In addition, extracts of apoptotic Jurkat cells were prepared following treatment with anti-Fas antibody (1 μg/ml) for three hours. To prepare the extracts, the cells were lysed in Triton X-100 buffer (1% Triton X-100, 25 mM Tris HCl) on ice for two hours and then microcentrifuged for 5 minutes. The soluble extract was retained (and was labeled TX100). Cells were lysed in cell extraction buffer with freeze/thawing. The soluble cytoplasmic fraction was set aside (and labeled CEB). Nuclear pellets from the preparation of the CEB cytoplasmic fraction were solubilized with Triton X-100 buffer, microcentrifuged, and the soluble fractions, which contains primarily nuclear DNA, was retained (and labeled CEB-TX100). Soluble cell extract was prepared by lysing cells with NP-40 buffer, followed by microcentrifugation for 5 minutes (and was labeled NP-40). *In vitro* cleavage was performed by incubating 16 μl of each extract (CEB, TX-100, CEB-TX100, and NP-40) with 4 μl of *in vitro* translated XIAP protein at 37°C for 7 hours. Negative controls, containing only TX100 buffer or CEB buffer were also

included. The proteins were separated on a 10% SDS-polyacrylamide gel, which was dried and exposed to X-ray film overnight.

In vitro cleavage of XIAP was apparent in the CEB extract. The observed molecular weight of the cleavage product was approximately 36 kDa (Fig. 17). The 10 kDa shift in the size of the cleavage product indicates that the observed product is derived from the amino-terminus of the recombinant protein, which contains six copies of the myc epitope (10 kDa). It thus appears that the cleavage product possesses at least two of the BIR domains, and that it is localized to the nucleus.

Example 5: Characterization of IAP Activity and Intracellular Localization Studies

The ability of IAPs to modulate apoptosis can be defined *in vitro* systems in which alterations of apoptosis can be detected. Mammalian expression constructs carrying IAP cDNAs, which are either full-length truncated, or antisense constructs can be introduced into cell lines such as CHO, NIH 3T3, HL60, Rat-1, or Jurkat cells. In addition, SF21 insect cells may be used, in which case the IAP gene is preferentially expressed using an insect heat shock promoter. Following transfection, apoptosis can be induced by standard methods, which include serum withdrawal, or application of staurosporine, menadione (which induces apoptosis via free radial formation), or anti-Fas antibodies. As a control, cells are cultured under the same conditions as those induced to undergo apoptosis, but either not transfected, or transfected with a vector that lacks an IAP insert. The ability of each IAP related construct to inhibit or enhance apoptosis upon expression can be quantified by calculating the survival index of the cells, i.e., the ratio of surviving transfected cells to surviving control cells. These

experiments can confirm the presence of apoptosis inhibiting activity and, as discussed below, can also be used to determine the functional region(s) of an IAP which may be employed to achieve enhancement of apoptosis. These assays may also be performed in combination with the application of additional compounds in order to identify compounds that enhance apoptosis via IAP expression.

Examples 6: Cell Survival Following Transfection with IAP Constructs and Induction of Apoptosis

Specific examples of the results obtained by performing various apoptosis suppression assays are shown in Figs. 10A to 10D. For example, CHO cell survival following transfection with one of six constructs and subsequent serum withdrawal is shown in Fig. 10A. The cells were transfected using Lipofectace™ with 2 μg of one of the following recombinant plasmids: pCDNA3-6myc-xiap (xiap), pCDNA3-6myc-hiap-1 (hiap-1), pCDNA3-6myc-hiap-2 (hiap-2), pCDNA3-bcl-2 (bcl-2), pCDNA3-HA-smn (smn), and pCDNA3-6myc (6-myc). Oligonucleotide primers were synthesized to allow PCR amplification and cloning of the xiap, hiap-1, and hiap-2 ORFs in pCDNA3 (Invitrogen). Each construct was modified to incorporate a synthetic myc tag encoding six repeats of the peptide sequence MEQKLISEEDL (SEQ ID NO:17), thus allowing detection of myc-IAP fusion proteins via monoclonal anti-myc antiserum (Egan et al., Nature 363:45-51, 1993). Triplicate samples of cell lines in 24-well dishes were washed 5 times with serum free media and maintained in serum free conditions during the course of the experiment. Cells that excluded trypan blue, and that were therefore viable, were counted with a hemocytometer immediately, 24 hours, 48 hours, and 72 hours, after serum withdrawal. Survival was calculated as a

percentage of the initial number of viable cells. In this experiment and those presented in Figs. 10B and 10D, the percentage of viable cells shown represents the average of three separate experiments performed in triplicate, +/- average deviation.

The survival of CHO cells following transfection (with each one of the six constructs described above) and exposure to menadione is shown in Fig. 10B. The cells were plated in 24-well dishes, allowed to grow overnight, and then exposed to 2O μM menadione for 1.5 hours (Sigma Chemical Co., St. Louis, MO). Triplicate samples were harvested at the time of exposure to menadione and 24 hours afterward, and survival was assessed by trypan blue exclusion.

The survival of Rat-1 cells following transfection (with each one of the six constructs described above) and exposure to staurosporine is shown in Fig. 10C. Rat-1 cells were transfected and then selected in medium containing 800 μg/ml G418 for two weeks. The cell line was assessed for resistance to staurosporine-induced apoptosis (1 μM) for 5 hours. Viable cells were counted 24 hours after exposure to staurosporine by trypan blue exclusion. The percentage of viable cells shown represents the average of two experiments, ± average deviation.

The Rat-1 cell line was also used to test the resistance of these cells to menadione (Fig. 10D) following transfection with each of the six constructs described above. The cells were exposed to 10 μM menadione for 1.5 hours, and the NUMBER of viable cells was counted 18 hours later.

Example 7: Comparison of Cell Survival Following Transfection with Full-length vs. Partial IAP Constructs

In order to investigate the mechanism whereby human IAPs, including XIAP, HIAP-1, and HIAP-2, afford protection against cell death, expression vectors were constructed that contained either: (1) full-length IAP cDNA (as described above), (2) a portion of an IAP gene that encodes the BIR domains, but not the RZF, or (3) a portion of an IAP gene that encodes the RZF, but not the BIR domains. Human and murine xiap cDNAs were tested by transient or stable expression in HeLa, Jurkat, and CHO cell lines. Following transfection, apoptosis was induced by serum withdrawal, application of menadione, or application of an anti-Fas antibody. Cell death was then assessed, as described above, by trypan blue exclusion. As a control for transfection efficiency, the cells were co-transfected with a β-gal expression construct. Typically, approximately 20% of the cells were successfully transfected.

When CHO cells were transiently transfected, constructs containing full-length human or mouse xiap cDNAs conferred modest but definite protection against cell death. In contrast, the survival of CHO cells transfected with constructs encoding only the BIR domains (i.e., lacking the RZF domain) was markedly enhanced 72 hours after serum deprivation. Furthermore, a large percentage of cells expressing the BIR domains were still viable after 96 hours, at which time no viable cells remained in the control, i.e., non-transfected, cell cultures, and less than 5% of the cells transfected with the vector only, i.e., lacking a cDNA insert, remained viable. Deletion of any of the BIR domains results in the complete loss of apoptotic suppression, which is reflected by a decrease in the

percentage of surviving CHO cells to control levels within 72 hours of serum withdrawal.

Stable pools of transfected CHO cells, which were maintained for several months under G418 selection, were induced to undergo apoptosis by exposure to 10 μM menadione for 2 hours. Among the CHO cells tested were those that were stably transfected with: (1) full-length murine xiap cDNA (miap), (2) full-length xiap cDNA (xiap), (3) full-length bcl-2 cDNA (Bcl-2), (4) cDNA encoding the three BIR domains (but not the RZF) of murine xiap (BIR), and (5) cDNA encoding the RZF (but not BIR domains) of m-xiap (RZF). Cells that were non-transfected (CHO) or transfected with the vector only (pcDNA3), served as controls for this experiment. Following exposure to 10 μM menadione, the transfected cells were washed with phosphate buffered saline (PBS) and cultured for an additional 24 hours in menadione-free medium. Cell death was assessed, as described above, by trypan blue exclusion. Less than 10% of the non-transfected or vector-only transfected cells remained viable at the end of the 24 hour survival period. Cells expressing the RZF did not fare significantly better. However, expression of full-length murine xiap, human xiap, or bcl-2, and expression of the BIR domains, enhanced cell survival. When the concentration of menadione was increased from 10 μM to 20 μM (with all other conditions of the experiment being the same as when 10 μM menadione was applied), the percentage of viable CHO cells that expressed the BIR domain cDNA construct was higher than the percentage of viable cells that expressed either full-length murine xiap or bcl-2.

Example 8: Analysis of the Subcellular Location of Expressed RZF and BIR Domains

The assays of cell death described above indicate that the RZF acts as a negative regulator of the anti-apoptotic function of IAPs. One way in which the RZF, and possibly other IAP domains, may exert their regulatory influence is by altering the expression of genes, whose products function in the apoptotic pathway.

In order to determine whether the subcellular locations of expressed RZF and BIR domains are consistent with roles as nuclear regulatory factors, COS cells were transiently transfected with the following four constructs, and the expressed polypeptide was localized by immunofluorescent microscopy: (1) pcDNA3-6myc-xiap, which encodes all 497 amino acids of SEQ ID NO:4, (2) pcDNA3-6myc-m-xiap, which encodes all 497 amino acids of mouse xiap (SEQ ID NO:10), (3) pcDNA3-6myc-mxiap-BIR, which encodes amino acids 1 to 341 of m-xiap (SEQ ID NO:10), and (4) pcDNA3-6myc-mxiap-RZF, which encodes amino acids 342-497 of murine xiap (SEQ ID NO:10). The cells were grown on multi-well tissue culture slides for 12 hours, and then fixed and permeabilized with methanol. The constructs used (here and in the cell death assays) were tagged with a human Myc epitope tag at the N-terminus. Therefore, a monoclonal anti-Myc antibody and a secondary goat anti-mouse antibody, which was conjugated to FITC, could be used to localize the expressed products in transiently transfected COS cells. Full-length XIAP and MIAP were located in the cytoplasm, with accentuated expression in the peri-nuclear zone. The same pattern of localization was observed when the cells expressed a construct encoding the RZF domain (but not the BIR domains). However, cells expressing the BIR

domains (without the RZF) exhibited, primarily, nuclear staining. The protein expressed by the BIR domain construct appeared to be in various stages of transfer to the nucleus.

These observations are consistent with the fact that, as described below, XIAP is cleaved within T cells that are treated with anti-Fas antibodies (which are potent inducers of apoptosis), and its N-terminal domain is translocated to the nucleus. As noted in Example 2 Hiap-2 appears to undergo a similar cleavage event.

Example 9: Testing of Antisense Oligonucleotides

1. Complete panel of adenovirus constructs. The panel may consist of approximately four types of recombinant virus. A) Sense orientation viruses for each of the IAP open reading frames. These viruses are designed to massively overexpress the recombinant protein in infected cells. XIAP, HIAP-1, HIAP-2, and NAIP. B) Antisense orientation viruses in which the viral promoter drives the synthesis of an mRNA of opposite polarity to the *iap* mRNA, thereby shutting off host cell synthesis of the targeted protein coding region. XIAP, HIAP-1, HIAP-2, and NAIP "antisense" constructs required. C) Sub-domain expression viruses. These constructs express only a partial IAP protein in infected cells. We have data indicating that deletion of the zinc finger of XIAP renders the protein more potent in protecting cell against apoptotic triggers. This data also indicates that expression of the zinc finger alone will indicate apoptosis by functioning as a dominant-negative repressor of XIAP function. XIAP-ΔZF and XIAP-Δbir viruses required. D) Control viruses. Functional analysis of the IAPs requires

suitable positive and negative controls for comparison. Bcl-2 sense, Bcl-2 antisense, p53 sense, and Lac Z (negative control) viruses may be utilized.

2. Confirmation of recombinant adenovirus function. Verification of the sense adenovirus function involves infection of tissue culture cells and determination of protein expression levels. We have performed western blot analysis of several of the recombinant adenoviruses, including NAIP, XIAP and XIAP-ΔZF. The remaining viruses may be ready readily assessed for protein expression using the polyclonal IAP antibodies. Functional analysis of the antisense viruses may be done at the RNA level using either northern blots of total RNA harvested from infected tissue culture cells or ribonuclease protection assays. Western blot analysis of infected cells will be used to determine whether the expressed antisense RNA interferes with IAP expression in the host cell.

3. Documentation that IAP overexpression results in increased drug resistance. We have optimized cell death assays to allow high through-put of samples with minimal sample variation. Testing of the sense IAP adenoviruses for their ability to alter drug sensitivity of breast and pancreatic adenocarcinoma cell lines may be accomplished as follows. Cancer cell lines are infected with the recombinant viruses, cultured for 5 days, then subdivided into 24 well plates. Triplicate cell receive increasing concentrations of the anti-cancer drug under investigation. Samples are harvested at 24, 48, and 72 hours post exposure, and assayed for the number of viable cells in the well. The dose response curve is then compared to uninfected and control virus (both positive and negative) infected cells. One may document a dramatic increase in the relative resistance of the cancer cell lines

when infected with the sense viruses, confirming our hypothesis that overexpression of the IAP proteins contributes to the anti-apoptotic phenotype of cancer cells. Initial experiments utilize the drugs doxorubicin, and adriamycin.

4. Documentation that antisense IAP overexpression results in increased drug sensitivity. Having confirmed that IAP overexpression renders cancer cell more resistant to chemo-therapeutic drugs, one may examine whether the antisense adenoviruses render the same cells more sensitive. The effectiveness of antisense IAP viruses relative to antisense Bcl-2 virus will also be assessed as a crucial milestone.

5. Identification of antisense oligonucleotides. Concomitant to the adenovirus work, we have designed a series of antisense oligonucleotides to various regions of each of the *iaps*. A generally accepted model of how antisense oligonucleotides function proposes that the formation of RNA/DNA duplexes in the nucleus activates cellular RnaseH enzymes which then enzymatically degrade the mRNA component of the hybrid. Virtually any region of the mRNA can be targeted, and therefore choosing an appropriate sequence to target is somewhat empirical. Many factors, including secondary structure of the target mRNA and the binding affinity of the targeted sequence determine whether a particular oligonucleotide will be effective, necessitating several oligos for each *iap*. Five oligonucleotides have been made for each *iap* mRNA based on the available computer algorhythms for predicting binding affinities and mRNA secondary structures. These and other

oligos may be tested for their ability to target their respective mRNAs for degradation using northern blot analysis.

6. *Optimization of oligonucleotides.* A secondary round of oligonucleotides may be made when effective target regions have been identified. These oligonucleotides target sequences in the immediate vicinity of the most active antisense oligonucleotides identified using methods such as those provided above. A second round of testing by northern blot analysis may be required.

7. *Testing antisense oligonucleotides in vitro.* Following successful identification and optimization of targeting oligonucleotides, one may test these in the tissue culture model system using the optimal cell lines such as those described in the cancer survey described herein. Experimental procedures may parallel those used in the recombinant antisense adenovirus work. Negative control oligonucleotides with miss-match sequences are used to establish base line or non-specific effects. Assisted transfection of the oligonucleotides using cationic lipid carriers may be compared to unassisted transfection. Confirmation of the effectiveness of specific antisense oligonucleotides prompts synthesis of oligos with modified phosphodiester linkages, such as phosphorothioate or methylimino substituted oligos. These may also be tested *in vitro*.

8. *Animal modeling of antisense oligonucleotide therapies.*
Animal modeling of the effectiveness of the antisense IAP approach is described here. Cell lines are routinely assessed for their tumorigenic potential in "nude" mice, a hairless strain of mouse that is immunocompromised, and thus extremely

susceptible to developing tumors. In the nude mouse assay, cancer cells are grown in tissue culture and then injected under the skin at multiple sites. The frequency with which these cells give rise to palpable tumors within a defined period of time provides an index of the tumorigenic potential of the cell line in the absence of interference by a functional immune system. Preliminary assessment of an antisense IAP therapeutic involves injection of cancer cells infected with the recombinant adenoviruses (sense, antisense, and control viruses) under the skin, and the tumorigenic index compared to that of untreated cells. One may also use this model to assess the effectiveness of systemic administration of antisense oligonucleotides in increasing the efficacy of anti-cancer drugs in the nude mouse model. Phosphorothioate or methylimino substituted oligos will be assessed at this stage. This type of antisense oligo has demonstrated enhanced cell permeability and slower clearance rates from the body in experimental animal models.

Example 10: Additional Apoptosis Assays

Specific examples of apoptosis assays are also provided in the following references. Assays for apoptosis in lymphocytes are disclosed by: Li et al., "Induction of apoptosis in uninfected lymphocytes by HIV-1 Tat protein", Science 268:429-431, 1995; Gibellini et al., "Tat-expressing Jurkat cells show an increased resistance to different apoptotic stimuli, including acute human immunodeficiency virus-type 1 (HIV-1) infection", Br. J. Haematol. 89:24-33, 1995; Martin et al., "HIV-1 infection of human $CD4^+$ T cells *in vitro*. Differential induction of apoptosis in these cells." J. Immunol. 152:330-42, 1994; Terai et al., "Apoptosis as a mechanism of cell death in cultured T lymphoblasts acutely

infected with HIV-1", J. Clin. Invest. 87:1710-5, 1991; Dhein et al., "Autocrine T-cell suicide mediated by APO-l/(Fas/CD95)11, Nature 373:438-441, 1995; Katsikis et al., "Fas antigen stimulation induces marked apoptosis of T lymphocytes in human immunodeficiency virus-infected individuals", J. Exp. Med. 1815:2029-2036, 1995; Westendorp et al., Sensitization of T cells to CD95-mediated apoptosis by HIV-1 Tat and gp12O", Nature 375:497, 1995; DeRossi et al., Virology 198:234-44, 1994.

Assays for apoptosis in fibroblasts are disclosed by: Vossbeck et al., "Direct transforming activity of TGF-beta on rat fibroblasts", Int. J. Cancer 61:92-97, 1995; Goruppi et al., "Dissection of c-myc domains involved in S phase induction of NIH3T3 fibroblasts", Oncogene 9:1537-44, 1994; Fernandez et al., "Differential sensitivity of normal and Ha-ras transformed C3H mouse embryo fibroblasts to tumor necrosis factor: induction of bcl-2, c-myc, and manganese superoxide dismutase in resistant cells", Oncogene 9:2009-17, 1994; Harrington et al., "c-Myc-induced apoptosis in fibroblasts is inhibited by specific cytokines", EMBO J., 13:3286-3295, 1994; Itoh et al., "A novel protein domain required for apoptosis. Mutational analysis of human Fas antigen", J. Biol. Chem. 268:10932-7, 1993.

Assays for apoptosis in neuronal cells are disclosed by: Melino et al., "Tissue transglutaminase and apoptosis: sense and antisense transfection studies with human neuroblastoma cells", Mol. Cell Biol. 14:6584-6596, 1994; Rosenbaum et al., "Evidence for hypoxia-induced, programmed cell death of cultured neurons", Ann. Neurol. 36:864-870, 1994; Sato et al., "Neuronal differentiation of PC12 cells as a result of prevention of cell death by bcl-2", J. Neurobiol. 25:1227-1234, 1994; Ferrari et al., "N-acetylcysteine D- and L-

stereoisomers prevents apoptotic death of neuronal cells", J. Neurosci. 1516:2857-2866, 1995; Talley et al., "Tumor necrosis factor alpha-induced apoptosis in human neuronal cells: protection by the antioxidant N-acetylcysteine and the genes bcl-2 and crmA", Mol. Cell Biol. 1585:2359-2366, 1995; Talley et al., "Tumor Necrosis Factor Alpha-Induced Apoptosis in Human Neuronal Cells: Protection by the Antioxidant NAcetylcysteine and the Genes bcl-2 and crma", Mol. Cell. Biol. 15:2359-2366, 1995; Walkinshaw et al., "Induction of apoptosis in catecholaminergic PC12 cells by L-DOPA. Implications for the treatment of Parkinson's disease.", J. Clin. Invest. 95:2458-2464, 1995.

Assays for apoptosis in insect cells are disclosed by: Clem et al., "Prevention of apoptosis by a baculovirus gene during infection of insect cells", Science 254:1388-90, 1991; Crook et al., "An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif", J. Virol. 67:2168-74, 1993; Rabizadeh et al., "Expression of the baculovirus p35 gene inhibits mammalian neural cell death", J. Neurochem. 61:2318-21, 1993; Birnbaum et al., "An apoptosis inhibiting gene from a nuclear polyhedrosis virus encoding a polypeptide with Cys/His sequence motifs", J. Virol. 68:2521-8, 1994; Clem et al., "Control of programmed cell death by the baculovirus genes p35 and IAP", Mol. Cell. Biol. 14:5212-5222, 1994.

Example 11: Construction of a Transgenic Animal

Characterization of IAP genes provided information that necessary for generation IAP transgenic animal models to be developed by homologous recombination (for knockouts) or transfection (for expression of IAP fragments, antisense IAP RNA, or increased expression of wild-type or mutant IAPs). Such models may be mammalian animal, e.g., a mouse. Such models are useful for the

identification of cancer therapeutics alone or in combination with cancer inducing cells or agents, or when such mice are crossed with mice genetically predisposed to cancers.

The preferred transgenic animal overexpression in IAP and has a predisposition to cancer. This mouse is particularly useful for the screening of potential cancer therapeutics.

Example 12: IAP Protein Expression

IAP genes and fragments thereof (i.e., RZF fragments) may be expressed in both prokaryotic and eukaryotic cell types. If an IAP fragment modulates apoptosis by exacerbating it, it may be desirable to express that protein under control of an inducible promoter.

In general, IAPs and fragments thereof may be produced by transforming a suitable host cell with all or part of the IAP-encoding cDNA fragment that has been placed into a suitable expression vector.

Those skilled in the art of molecular biology will understand that a wide variety of expression systems may be used to produce the recombinant protein. The precise host cell used is not critical to the invention, although cancer cells are preferable. The IAP protein may be produced in a prokaryotic host (e.g., *E. coli*) or in a eukaryotic host (e.g., *S. cerevisiae*, insect cells such as Sf21 cells, or mammalian cells such as COS-1, NIH 3T3, or HeLa cells, or other highly proliferative cell types). These cells are publically available, for example, from the American Type Culture Collection, Rockville, MD; see also Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, New York, NY, 1994). The method of transduction and the choice of expression vehicle will

depend on the host system selected. Transformation and transfection methods are described, e.g., in Ausubel et al. (*supra*), and expression vehicles may be chosen from those provided, e.g., in Cloning Vectors: A Laboratory Manual (P.H. Pouwels et al., 1985, Supp. 1987).

Polypeptides of the invention, particularly short IAP fragments, can also be produced by chemical synthesis (e.g., by the methods described in Solid Phase Peptide Synthesis, 2nd ed., 1984 The Pierce Chemical Co., Rockford, IL). These general techniques of polypeptide expression and purification can also be used to produce and isolate useful IAP fragments or analogs, as described herein.

Example 13: Anti-IAP Antibodies

In order to generate IAP-specific antibodies, an IAP coding sequence (e.g., amino acids 180-276) can be expressed as a C-terminal fusion with glutathione S-transferase (GST; Smith et al., Gene 67:31-40, 1988). The fusion protein can be purified on glutathione-Sepharose beads, eluted with glutathione, and cleaved with thrombin (at the engineered cleavage site), and purified to the degree required to successfully immunize rabbits. Primary immunizations can be carried out with Freund's complete adjuvant and subsequent immunizations performed with Freund's incomplete adjuvant. Antibody titres are monitored by Western blot and immunoprecipitation analyses using the thrombin-cleaved IAP fragment of the GST-IAP fusion protein. Immune sera are affinity purified using CNBr-Sepharose-coupled IAP protein. Antiserum specificity is determined using a panel of unrelated GST proteins (including GSTp53, Rb, HPV-16 E6, and E6-AP) and GST-trypsin (which was generated by PCR using known sequences).

As an alternate or adjunct immunogen to GST fusion proteins, peptides corresponding to relatively unique hydrophilic regions of IAP may be generated and coupled to keyhole limpet hemocyanin (KLH) through an introduced C-terminal lysine. Antiserum to each of these peptides is similarly affinity purified on peptides conjugated to BSA, and specificity is tested by ELISA and Western blotting using peptide conjugates, and by Western blotting and immunoprecipitation using IAP expressed as a GST fusion protein.

Alternatively, monoclonal antibodies may be prepared using the IAP proteins described above and standard hybridoma technology (see, e.g., Kohler et al., Nature 256:495, 1975; Kohler et al., Eur. J. Immunol. 6:511, 1976; Kohler et al., Eur. J. Immunol. 6:292, 1976; Hammerling et al., In Monoclonal Antibodies and T Cell Hybridomas, Elsevier, New York, NY, 1981; Ausubel et al., *supra*). Once produced, monoclonal antibodies are also tested for specific IAP recognition by Western blot or immunoprecipitation analysis (by the methods described in Ausubel et al., *supra*).

Antibodies that specifically recognize IAPs or fragments of IAPs, such as those described herein containing one or more BIR domains (but not a ring zinc finger domain), or that contain a ring zinc finger domain (but not a BIR domain) are considered useful in the invention. They may, for example, be used in an immunoassay to monitor IAP expression levels or to determine the subcellular location of an IAP or IAP fragment produced by a mammal. Antibodies that inhibit the 26 kDa IAP cleavage product described herein (which contains at least one BIR domain) may be especially useful in inducing apoptosis in cells undergoing undesirable proliferation.

Preferably, antibodies of the invention are produced using IAP sequence that does not reside within highly conserved regions, and that appears likely to be antigenic, as analyzed by criteria such as those provided by the Peptide structure program (Genetics Computer Group Sequence Analysis Package, Program Manual for the GCG Package, Version 7, 1991) using the algorithm of Jameson and Wolf (CABIOS 4:181, 1988). Specifically, these regions, which are found between BIR1 and BIR2 of all IAPs, are: from amino acid 99 to amino acid 170 of hiap-1, from amino acid 123 to amino acid 184 of hiap-2, and from amino acid 116 to amino acid 133 of either xiap or m-xiap. These fragments can be generated by standard techniques, e.g., by the PCR, and cloned into the pGEX expression vector (Ausubel et al., *supra*). Fusion proteins are expressed in *E. coli* and purified using a glutathione agarose affinity matrix as described in Ausubel et al. (*supra*). In order to minimize the potential for obtaining antisera that is non-specific, or exhibits low-affinity binding to IAP, two or three fusions are generated for each protein, and each fusion is injected into at least two rabbits. Antisera are raised by injections in series, preferably including at least three booster injections.

Example 14: Identification of Molecules That Modulate IAP Protein Expression

IAP cDNAs facilitate the identification of molecules that decrease IAP expression or otherwise enhance apoptosis normally blocked by the IAPs. In one approach, candidate molecules are added, in varying concentration, to the culture medium of cells expressing IAP mRNA. IAP expression is then measured, for example, by Northern blot analysis (Ausubel et al., *supra*) using an IAP cDNA, or cDNA fragment, as a hybridization probe. The level of IAP expression in the presence of the candidate molecule is compared to the level of IAP

expression in the absence of the candidate molecule, all other factors (e.g., cell type and culture conditions) being equal.

The effect of candidate molecules on IAP-mediated apoptosis may, instead, be measured at the level of IAP protein or level of IAP fragments using the general approach described above with standard protein detection techniques, such as Western blotting or immunoprecipitation with an IAP-specific antibody (for example, the IAP antibodies described herein).

Compounds that modulate the level of IAP may be purified, or substantially purified, or may be one component of a mixture of compounds such as an extract or supernatant obtained from cells (Ausubel et al., *supra*). In an assay of a mixture of compounds, IAP expression is tested against progressively smaller subsets of the compound pool (e.g., produced by standard purification techniques such as HPLC or FPLC) until a single compound or minimal number of effective compounds is demonstrated to modulate IAP expression.

Compounds may also be screened for their ability to enhance IAP-mediated apoptosis. In this approach, the degree of apoptosis in the presence of a candidate compound is compared to the degree of apoptosis in its absence, under equivalent conditions. Again, the screen may begin with a pool of candidate compounds, from which one or more useful modulator compounds are isolated in a step-wise fashion. Apoptosis activity may be measured by any standard assay, for example, those described herein.

Another method for detecting compounds that modulate the activity of IAPs is to screen for compounds that interact physically with a given IAP polypeptide. These compounds may be detected by adapting interaction trap expression systems known in the art. These systems detect protein interactions

using a transcriptional activation assay and are generally described by Gyuris et al. (Cell 75:791-803, 1993) and Field et al. (Nature 340:245-246, 1989), and are commercially available from Clontech (Palo Alto, CA). In addition, PCT Publication WO 95/28497 describes an interaction trap assay in which proteins involved in apoptosis, by virtue of their interaction with Bcl-2, are detected. A similar method may be used to identify proteins and other compounds that interact with IAPs.

Compounds or molecules that function as modulators of IAP-mediated cell death may include peptide and non-peptide molecules such as those present in cell extracts, mammalian serum, or growth medium in which mammalian cells have been cultured.

TABLE 2

OLIGONUCLEOTIDE PRIMERS FOR THE SPECIFIC RT-PCR AMPLIFICATION OF IAP GENES

IAP Gene	Forward Primer (nucleotide position*)	Reverse Primer (nucleotide position*)	Size of Product (bp)
h-xiap	p2415 (876-896)	p2449 (1291-1311)	435
m-xiap	p2566 (458-478)	p2490 (994-1013)	555
h-hiap1	p2465 (827-847)	p2464 (1008-1038)	211
m-hiap1	p2687 (747-767)	p2684 (1177-1197)	450
hiap2	p2595 (1562-1585)	p2578 (2339-2363)	801[a] 618[b]
m-hiap2	p2693 (1751-1772)	p2734 (2078-2100)	349

* Nucleotide position as determined from Figs. 1-4 for each IAP gene

[a] PCR product size of hiap2a

[b] PCR product size of hiap2b

Example 15: Assignment of xiap, hiap-1 and hiap-2 to Chromosomes Xq25 and 11q22-23 by Fluorescence *in Situ* Hybridization (FISH)

Fluorescence *in situ* hybridization (FISH) was used to identify the chromosomal location of xiap, hiap-1 and hiap-2.

A total of 101 metaphase spreads were examined with the xiap probe, as described above. Symmetrical fluorescent signals on either one or both homologs of chromosome Xq25 were observed in 74% of the cells analyzed. Following staining with hiap-1 and hiap-2 probes, 56 cells were analyzed and doublet signals in the region 11q22-23 were observed in 83% of cells examined.

The xiap gene was mapped to Xq25 while the hiap-1 and hiap-2 genes were mapped at the border of 11q22 and 11q23 bands.

These experiments confirmed the location of the xiap gene on chromosome Xq25. No highly consistent chromosomal abnormalities involving band Xq25 have been reported so far in any malignancies. However, deletions within this region are associated with a number of immune system defects including X-linked lymphoproliferative disease (Wu et al., Genomics 17:163-170, 1993).

Cytogenetic abnormalities of band 11q23 have been identified in more than 50% of infant leukemias regardless of the phenotype (Martinez-Climet et al., Leukaemia 9:1299-1304, 1995). Rearrangements of the MLL Gene (mixed lineage leukemia or myeloid lymphoid leukemia; Ziemin Van der Poel et al., Proc. Natl. Acad. Sci. USA 88:10735-10739, 1991) have been detected in 80% of cases with 11q23 translocation, however patients whose rearrangements clearly involved regions other than the MLL gene were also reported (Kobayashi et al., Blood 82:547-551, 1993). Thus, the IAP genes may follow the Bcl-2 paradigm, and would therefore play an important role in cancer transformation.

<u>Incorporation by Reference</u>

The following documents and all the references referred to herein are incorporated by reference: U.S.S.N. 08/511,485, filed August 4, 1995; U.S.S.N. 08/576,956, filed December 22, 1995; PCT/IB96/01022, filed August 5, 1996; U.S.S.N. 60/017,354, filed April 26, 1996; U.S.S.N. 60/030,931, filed November 15, 1996 (Express Mail Labeling Number RB794124826US); U.S.S.N. 60/030,590, filed November 14, 1996 (Express Mail Labeling Number

RB794124804US); U.S. Patent No. 5,576,208, issued November 19, 1996; and PCT Application IB97/00142, filed January 17, 1997 claiming priority from UK 9601108.5, filed January 19, 1996.

Other Embodiments

In other embodiments, the invention includes use of any protein which is substantially identical to a mammalian IAP polypeptides (Figs. 1-6; SEQ ID NOs:1-42); such homologs include other substantially pure naturally-occurring mammalian IAP proteins as well as allelic variants; natural mutants; induced mutants; DNA sequences which encode proteins and also hybridize to the IAP DNA sequences of Figs. 1-6 (SEQ ID NOS:1-42) under high stringency conditions or, less preferably, under low stringency conditions (e.g., washing at 2X SSC at 40°C with a probe length of at least 40 nucleotides); and proteins specifically bound by antisera directed to a IAP polypeptide. The term also includes chimeric polypeptides that include a IAP portion.

The invention further includes use of analogs of any naturally-occurring IAP polypeptide. Analogs can differ from the naturally-occurring IAP protein by amino acid sequence differences, by post-translational modifications, or by both. Analogs of the invention will generally exhibit at least 85%, more preferably 90%, and most preferably 95% or even 99% identity with all or part of a naturally occurring IAP amino acid sequence. The length of sequence comparison is at least 15 amino acid residues, preferably at least 25 amino acid residues, and more preferably more than 35 amino acid residues. Modifications include *in vivo* and *in vitro* chemical derivatization of polypeptides, e.g., acetylation, carboxylation, phosphorylation, or glycosylation; such modifications

may occur during polypeptide synthesis or processing or following treatment with isolated modifying enzymes. Analogs can also differ from the naturally-occurring IAP polypeptide by alterations in primary sequence. These include genetic variants, both natural and induced (for example, resulting from random mutagenesis by irradiation or exposure to ethanemethylsulfate or by site-specific mutagenesis as described in Sambrook, Fritsch and Maniatis, Molecular Cloning: A Laboratory Manual (2d ed.), CSH Press, 1989, or Ausubel et al., *supra*). Also included are cyclized peptides, molecules, and analogs which contain residues other than L-amino acids, e.g., D-amino acids or nonnaturally occurring or synthetic amino acids, e.g., B or y amino acids. In addition to full-length polypeptides, the invention also includes IAP polypeptide fragments. As used herein, the term "fragment," means at least 20 contiguous amino acids, preferably at least 30 contiguous amino acids, more preferably at least 50 contiguous amino acids, and most preferably at least 60 to 80 or more contiguous amino acids. Fragments of IAP polypeptides can be generated by methods known to those skilled in the art or may result from normal protein processing (e.g., removal of amino acids from the nascent polypeptide that are not required for biological activity or removal of amino acids by alternative mRNA splicing or alternative protein processing events).

Preferable fragments or analogs used according to the methods of the invention are those which facilitate specific detection of a IAP nucleic acid or amino acid sequence in a sample to be diagnosed. Particularly useful IAP fragments for this purpose include, without limitation, the amino acid fragments shown in Table 2.

The methods of the invention may use antibodies prepared by a variety of methods. For example, the IAP or NAIP polypeptide, or antigenic fragments thereof, can be administered to an animal in order to induce the production of polyclonal antibodies. Alternatively, antibodies used as described herein may be monoclonal antibodies, which are prepared using hybridoma technology (see, e.g., Kohler et al., Nature 256:495, 1975; Kohler et al., Eur. J. Immunol. 6:511, 1976; Kohler et al., Eur. J. Immunol. 6:292, 1976; Hammerling et al., In Monoclonal Antibodies and T Cell Hybridomas, Elsevier, NY, 1981). The invention features use of antibodies that specifically bind human or murine IAP or NAIP polypeptides, or fragments thereof. In particular the invention features "neutralizing" antibodies. By "neutralizing" antibodies is meant antibodies that interfere with any of the biological activities of IAP or NAIP polypeptides, particularly the ability of IAPs to inhibit apoptosis. The neutralizing antibody may reduce the ability of IAP polypeptides to inhibit polypeptides by, preferably 50%, more preferably by 70%, and most preferably by 90% or more. Any standard assay of apoptosis, including those described herein, by those incorporated by reference and those in the art, may be used to assess neutralizing antibodies.

In addition to intact monoclonal and polyclonal anti-IAP antibodies, the invention features use of various genetically engineered antibodies, humanized antibodies, and antibody fragments, including F(ab')2, Fab', Fab, Fv and sFv fragments. Antibodies can be humanized by methods known in the art, e.g., monoclonal antibodies with a desired binding specificity can be commercially humanized (Scotgene, Scotland; Oxford Molecular, Palo Alto, CA). Fully human

antibodies, such as those expressed in transgenic animals, are also features of the invention (Green et al., Nature Genetics 7:13-21, 1994).

Ladner (U.S. Patent Nos. 4,946,778 and 4,704,692) describes methods for preparing single polypeptide chain antibodies. Ward et al. (Nature 341:544-546, 1989) describe the preparation of heavy chain variable domains, which they term "single domain antibodies," which have high antigen-binding affinities. McCafferty et al. (Nature 348:552-554, 1990) show that complete antibody V domains can be displayed on the surface of fd bacteriophage, that the phage bind specifically to antigen, and that rare phage (one in a million) can be isolated after affinity chromatography. Boss et al. (U.S. Patent 4,816,397) describe various methods for producing immunoglobulins, and immunologically functional fragments thereof, which include at least the variable domains of the heavy and light chain in a single host cell. Cabilly et al. (U.S. Patent 4,816,567) describe methods for preparing chimeric antibodies.

What is claimed is: